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 NEWS  1           Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2  Jan 25   BLAST(R) searching in REGISTRY available in STN on the Web
 NEWS  3  Jan 29   FSTA has been reloaded and moves to weekly updates
 NEWS  4  Feb 01   DKILIT now produced by FIZ Karlsruhe and has a new update
                   frequency
 NEWS  5  Feb 19   Access via Tymnet and SprintNet Eliminated Effective 3/31/02
 NEWS  6  Mar 08   Gene Names now available in BIOSIS
 NEWS  7  Mar 22   TOXLIT no longer available
 NEWS  8  Mar 22   TRCTHERMO no longer available
 NEWS  9  Mar 28   US Provisional Priorities searched with P in CA/CAplus
                   and USPATFULL
 NEWS 10  Mar 28   LIPINSKI/CALC added for property searching in REGISTRY
 NEWS 11  Apr 02   PAPERCHEM no longer available on STN.  Use PAPERCHEM2 instead.
 NEWS 12  Apr 08   "Ask CAS" for self-help around the clock
 NEWS 13  Apr 09   BEILSTEIN: Reload and Implementation of a New Subject Area
 NEWS 14  Apr 09   ZDB will be removed from STN
 NEWS 15  Apr 19   US Patent Applications available in IFICDB, IFIPAT, and IFIUDB
 NEWS 16  Apr 22   Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
 NEWS 17  Apr 22   BIOSIS Gene Names now available in TOXCENTER
 NEWS 18  Apr 22   Federal Research in Progress (FEDRIP) now available

 NEWS EXPRESS  February 1 CURRENT WINDOWS VERSION IS V6.0d,
               CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP),
               AND CURRENT DISCOVER FILE IS DATED 05 FEBRUARY 2002
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 NEWS INTER    General Internet Information
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FILE 'HOME' ENTERED AT 15:41:16 ON 09 MAY 2002

=> file .biotech
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
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=> s gene expression
   4 FILES SEARCHED...
L1      700092 GENE EXPRESSION

=> s cluster analysis
L2       21071 CLUSTER ANALYSIS

=> s l1 and l2
L3         577 L1 AND L2

=> array
ARRAY IS NOT A RECOGNIZED COMMAND
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"HELP COMMANDS" at an arrow prompt (=>).

=> s array
L4      129141 ARRAY

=> s l3 and l4
L5         183 L3 AND L4

=> s microarray
L6       12481 MICROARRAY

=> s l5 and l6
L7          95 L5 AND L6

=> sl7 not p7>1999
SL7 IS NOT A RECOGNIZED COMMAND
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"HELP COMMANDS" at an arrow prompt (=>).

=> s l7 not py>1999
L8           0 L7 NOT PY>1999

=> s l7 not py>1998
L9           0 L7 NOT PY>1998

=> dup rem l7
PROCESSING COMPLETED FOR L7
L10          80 DUP REM L7 (15 DUPLICATES REMOVED)

=> d ti l10 1-30
```

L10 ANSWER 1 OF 80 MEDLINE
TI Differential gene regulation by the two progesterone receptor isoforms in human breast cancer cells.

L10 ANSWER 2 OF 80 MEDLINE
TI DNA **microarray** analysis of differential **gene expression** in Borrelia burgdorferi, the Lyme disease spirochete.

L10 ANSWER 3 OF 80 MEDLINE
TI Identifying pre-post chemotherapy differences in **gene expression** in breast tumours: a statistical method appropriate for this aim.

L10 ANSWER 4 OF 80 MEDLINE DUPLICATE 1
TI High-density **microarray** analysis of hippocampal **gene expression** following experimental brain injury.

L10 ANSWER 5 OF 80 MEDLINE
TI **Gene expression** profiling predicts clinical outcome of breast cancer.

L10 ANSWER 6 OF 80 MEDLINE
TI Genome-wide cDNA **microarray** screening to correlate **gene expression** profiles with sensitivity of 85 human cancer xenografts to anticancer drugs.

L10 ANSWER 7 OF 80 MEDLINE
TI Global **gene expression** profiling in Barrett's esophagus and esophageal cancer: a comparative analysis using cDNA microarrays.

L10 ANSWER 8 OF 80 MEDLINE DUPLICATE 2
TI **Microarray** detection of **gene expression** changes induced by 1,25(OH)(2)D(3) and a Ca(2+) influx-activating analog in osteoblastic ROS 17/2.8 cells.

L10 ANSWER 9 OF 80 MEDLINE DUPLICATE 3
TI Expression of cytokine- and chemokine-related genes in peripheral blood mononuclear cells from lupus patients by cDNA **array**.

L10 ANSWER 10 OF 80 MEDLINE
TI Global **gene expression** analysis of gastric cancer by oligonucleotide microarrays.

L10 ANSWER 11 OF 80 MEDLINE
TI The advantages of cDNA **microarray** as an effective tool for identification of reproductive organ-specific genes in a model legume, Lotus japonicus.

L10 ANSWER 12 OF 80 MEDLINE
TI Screening of **gene expression** profiles in gastric epithelial cells induced by Helicobacter pylori using **microarray** analysis.

L10 ANSWER 13 OF 80 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Identification of genes differentially expressed in cultured human osteoblasts versus human fibroblasts by DNA **microarray** analysis.

L10 ANSWER 14 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Methods for gene profiling arrays involving RNA or cDNA amplification

L10 ANSWER 15 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Method for selecting differentially expressed genes for use in informative nucleic acid arrays

L10 ANSWER 16 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Methods for **gene expression** profiling to diagnose disease, monitor drug therapy, identify physiological states, and identify differentially expressed genes in secretory versus proliferative endometrium

L10 ANSWER 17 OF 80 MEDLINE DUPLICATE 4
TI Bootstrapping **cluster analysis**: assessing the reliability of conclusions from **microarray** experiments.

L10 ANSWER 18 OF 80 MEDLINE
TI The consequences of chromosomal aneuploidy on **gene expression** profiles in a cell line model for prostate carcinogenesis.

L10 ANSWER 19 OF 80 MEDLINE
TI Estrogen receptor status in breast cancer is associated with remarkably distinct **gene expression** patterns.

L10 ANSWER 20 OF 80 MEDLINE DUPLICATE 5
TI Molecular profiling of transformed and metastatic murine squamous carcinoma cells by differential display and cDNA **microarray** reveals altered expression of multiple genes related to growth, apoptosis, angiogenesis, and the NF-kappaB signal pathway.

L10 ANSWER 21 OF 80 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 6
TI Papillomavirus type 16 oncogenes downregulate expression of interferon-responsive genes and upregulate proliferation-associated and NF-.kappa.B-responsive genes in cervical keratinocytes

L10 ANSWER 22 OF 80 MEDLINE
TI DNA **microarray** analysis of genes involved in p53 mediated apoptosis: activation of Apaf-1.

L10 ANSWER 23 OF 80 MEDLINE
TI New molecular phenotypes in the dst mutants of Arabidopsis revealed by DNA **microarray** analysis.

L10 ANSWER 24 OF 80 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI High-sensitivity **array** analysis of **gene expression** for the early detection of disseminated breast tumor cells in peripheral blood.

L10 ANSWER 25 OF 80 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Identification of **gene expression** patterns in superficial and invasive human bladder cancer.

L10 ANSWER 26 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI **Gene expression** in 1-trial learning of a conditioned taste aversion.

L10 ANSWER 27 OF 80 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Distinct **gene expression** profiling in chronic lymphocytic leukemia with 11q23 deletion.

L10 ANSWER 28 OF 80 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
TI **Gene expression** profiling of B cell chronic lymphocytic leukemia reveals a homogenous phenotype related to memory B cells;
cluster analysis, DNA chip, and DNA **microarray**

L10 ANSWER 29 OF 80 CAPLUS COPYRIGHT 2002 ACS

TI Establishment of normal, terminally differentiating mouse erythroid progenitors: molecular characterization by cDNA arrays

L10 ANSWER 30 OF 80 MEDLINE
TI RNA expression in the early characterization of hepatotoxicants in Wistar rats by high-density DNA microarrays.

=> d ibib abs l10 1-10

L10 ANSWER 1 OF 80 MEDLINE
ACCESSION NUMBER: 2002106152 MEDLINE
DOCUMENT NUMBER: 21826375 PubMed ID: 11717311
TITLE: Differential gene regulation by the two progesterone receptor isoforms in human breast cancer cells.
AUTHOR: Richer Jennifer K; Jacobsen Britta M; Manning Nicole G; Abel M Greg; Wolf Douglas M; Horwitz Kathryn B
CORPORATE SOURCE: Department of Medicine/Endocrinology, University of Colorado School of Medicine, Denver, Colorado 80262, USA.. jennifer.richer@uchsc.edu
CONTRACT NUMBER: CA26869 (NCI)
DK48238 (NIDDK)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2002 Feb 15) 277 (7) 5209-18.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200203
ENTRY DATE: Entered STN: 20020212
Last Updated on STN: 20020322
Entered Medline: 20020321
AB The PR-A and PR-B isoforms of progesterone receptors (PR) have different physiological functions, and their ratio varies widely in breast cancers. To determine whether the two PR regulate different genes, we used human breast cancer cell lines engineered to express one or the other isoform. Cells were treated with progesterone in triplicate, time-separated experiments, allowing statistical analyses of **microarray gene expression** data. Of 94 progesterone-regulated genes, 65 are uniquely regulated by PR-B, 4 uniquely by PR-A, and only 25 by both. Almost half the genes encode proteins that are membrane-bound or involved in membrane-initiated signaling. We also find an important set of progesterone-regulated genes involved in mammary gland development and/or implicated in breast cancer. This first, large scale study of PR gene regulation has important implications for the measurement of PR in breast cancers and for the many clinical uses of synthetic progestins. It suggests that it is important to distinguish between the two isoforms in breast cancers and that isoform-specific genes can be used to screen for ligands that selectively modulate the activity of PR-A or PR-B. Additionally, use of natural target genes, rather than "consensus" response elements, for transcription studies should improve our understanding of steroid hormone action.

L10 ANSWER 2 OF 80 MEDLINE
ACCESSION NUMBER: 2002111052 MEDLINE
DOCUMENT NUMBER: 21819468 PubMed ID: 11830671
TITLE: DNA **microarray** analysis of differential **gene expression** in Borrelia burgdorferi, the Lyme disease spirochete.
AUTHOR: Revel Andrew T; Talaat Adel M; Norgard Michael V
CORPORATE SOURCE: Department of Microbiology, University of Texas Southwestern Medical Center, Dallas, TX 75390, USA.
CONTRACT NUMBER: AI-45538 (NIAID)

SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2002 Feb 5) 99 (3) 1562-7. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200203
ENTRY DATE: Entered STN: 20020215
Last Updated on STN: 20020308
Entered Medline: 20020307

AB DNA microarrays were used to survey the adaptive genetic responses of Borrelia burgdorferi (Bb) B31, the Lyme disease spirochete, when grown under conditions analogous to those found in unfed ticks (UTs), fed ticks (FTs), or during mammalian host adaptation (Bb in dialysis membrane chambers implanted in rats). Microarrays contained 95.4% of the predicted B31 genes, 150 (8.6%) of which were differentially regulated (changes of > or = 1.8-fold) among the three growth conditions. A substantial proportion (46%) of the differentially regulated genes encoded proteins with predicted export signals (29% from predicted lipoproteins), emphasizing the importance to Bb of modulating its extracellular proteome. For B31 cultivated at the more restrictive UT condition, **microarray** data provided evidence of a bacterial stringent response and factors that restrict cell division. A large proportion of genes were responsive to the FT growth condition, wherein increased temperature and reduced pH were prominent environmental parameters. A surprising theme, supported by **cluster analysis**, was that many of the **gene expression** changes induced during the FT growth condition were transient and largely tempered as B31 adapted to the mammalian host, suggesting that once Bb gains entry and adapts to mammalian tissues, fewer differentially regulated genes are exploited. It therefore would seem that although widely dissimilar, the UT and dialysis membrane chamber growth conditions promote more static patterns of **gene expression** in Bb. The **microarray** data thus provide a basis for formulating new testable hypotheses regarding the life cycle of Bb and attaining a more complete understanding of many aspects of Bb's complex parasitic strategies.

L10 ANSWER 3 OF 80 MEDLINE
ACCESSION NUMBER: 2002216642 MEDLINE
DOCUMENT NUMBER: 21949770 PubMed ID: 11953855
TITLE: Identifying pre-post chemotherapy differences in **gene expression** in breast tumours: a statistical method appropriate for this aim.
AUTHOR: Korn E L; McShane L M; Troendle J F; Rosenwald A; Simon R
CORPORATE SOURCE: Biometric Research Branch, EPN-8128, National Cancer Institute, National Institutes of Health, Bethesda MD 20892, USA.. korne@ctep.nci.nih.gov
SOURCE: BRITISH JOURNAL OF CANCER, (2002 Apr 8) 86 (7) 1093-6. Journal code: 0370635. ISSN: 0007-0920.
PUB. COUNTRY: Scotland: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020416
Last Updated on STN: 20020501
Entered Medline: 20020430

AB Although widely used for the analysis of **gene expression** **microarray** data, **cluster analysis** may not be the most appropriate statistical technique for some study aims. We demonstrate this by considering a previous analysis of **microarray** data obtained on breast tumour specimens, many of which were paired specimens from the same patient before and after chemotherapy. Reanalysing

the data using statistical methods that appropriately utilise the paired differences for identification of differentially expressed genes, we find 17 genes that we can confidently identify as more expressed after chemotherapy than before. These findings were not reported by the original investigators who analysed the data using **cluster analysis** techniques.

L10 ANSWER 4 OF 80 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2002159238 MEDLINE
DOCUMENT NUMBER: 21888965 PubMed ID: 11891777
TITLE: High-density **microarray** analysis of hippocampal **gene expression** following experimental brain injury.
AUTHOR: Matzilevich David A; Rall Jason M; Moore Anthony N; Grill Raymond J; Dash Pramod K
CORPORATE SOURCE: The Vivian L. Smith Center for Neurologic Research, Departments of Neurobiology and Anatomy, Neurosurgery, The University of Texas Medical School, Houston, Texas 77225, USA.
CONTRACT NUMBER: MH49662 (NIMH)
NS3545 (NINDS)
P50NS23327 (NINDS)
SOURCE: JOURNAL OF NEUROSCIENCE RESEARCH, (2002 Mar 1) 67 (5) 646-63.
Journal code: 7600111. ISSN: 0360-4012.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020314
Last Updated on STN: 20020501
Entered Medline: 20020430
AB Behavioral, biophysical, and pharmacological studies have implicated the hippocampus in the formation and storage of spatial memory. Traumatic brain injury (TBI) often causes spatial memory deficits, which are thought to arise from the death as well as the dysfunction of hippocampal neurons. Cell death and dysfunction are commonly associated with and often caused by altered expression of specific genes. The identification of the genes involved in these processes, as well as those participating in postinjury cellular repair and plasticity, is important for the development of mechanism-based therapies. To monitor the expression levels of a large number of genes and to identify genes not previously implicated in TBI pathophysiology, a high-density oligonucleotide **array** containing 8,800 genes was interrogated. RNA samples were prepared from ipsilateral hippocampi 3 hr and 24 hr following lateral cortical impact injury and compared to samples from sham-operated controls. **Cluster analysis** was employed using statistical algorithms to arrange the genes according to similarity in patterns of expression. The study indicates that the genomic response to TBI is complex, affecting approximately 6% (at the time points examined) of the total number of genes examined. The identity of the genes revealed that TBI affects many aspects of cell physiology, including oxidative stress, metabolism, inflammation, structural changes, and cellular signaling. The analysis revealed genes whose expression levels have been reported to be altered in response to injury as well as several genes not previously implicated in TBI pathophysiology.

L10 ANSWER 5 OF 80 MEDLINE
ACCESSION NUMBER: 2002099463 MEDLINE
DOCUMENT NUMBER: 21681887 PubMed ID: 11823860
TITLE: **Gene expression** profiling predicts clinical outcome of breast cancer.
COMMENT: Comment in: Nature. 2002 Jan 31;415(6871):484-5

AUTHOR: van 't Veer Laura J; Dai Hongyue; van de Vijver Marc J; He Yudong D; Hart Augustinus A M; Mao Mao; Peterse Hans L; van der Kooy Karin; Marton Matthew J; Witteveen Anke T; Schreiber George J; Kerkhoven Ron M; Roberts Chris; Linsley Peter S; Bernards Rene; Friend Stephen H

CORPORATE SOURCE: Division of Diagnostic Oncology, The Netherlands Cancer Institute, 121 Plesmanlaan, 1066 CX Amsterdam, The Netherlands.

SOURCE: NATURE, (2002 Jan 31) 415 (6871) 530-6.
Journal code: 0410462. ISSN: 0028-0836.

PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200203

ENTRY DATE: Entered STN: 20020207
Last Updated on STN: 20020313
Entered Medline: 20020312

AB Breast cancer patients with the same stage of disease can have markedly different treatment responses and overall outcome. The strongest predictors for metastases (for example, lymph node status and histological grade) fail to classify accurately breast tumours according to their clinical behaviour. Chemotherapy or hormonal therapy reduces the risk of distant metastases by approximately one-third; however, 70-80% of patients receiving this treatment would have survived without it. None of the signatures of breast cancer **gene expression** reported to date allow for patient-tailored therapy strategies. Here we used DNA **microarray** analysis on primary breast tumours of 117 young patients, and applied supervised classification to identify a **gene expression** signature strongly predictive of a short interval to distant metastases ('poor prognosis' signature) in patients without tumour cells in local lymph nodes at diagnosis (lymph node negative). In addition, we established a signature that identifies tumours of BRCA1 carriers. The poor prognosis signature consists of genes regulating cell cycle, invasion, metastasis and angiogenesis. This **gene expression** profile will outperform all currently used clinical parameters in predicting disease outcome. Our findings provide a strategy to select patients who would benefit from adjuvant therapy.

L10 ANSWER 6 OF 80 MEDLINE

ACCESSION NUMBER: 2002082994 MEDLINE

DOCUMENT NUMBER: 21668025 PubMed ID: 11809704

TITLE: Genome-wide cDNA **microarray** screening to correlate **gene expression** profiles with sensitivity of 85 human cancer xenografts to anticancer drugs.

AUTHOR: Zembutsu Hitoshi; Ohnishi Yasuyuki; Tsunoda Tatsuhiko; Furukawa Yoichi; Katagiri Toyomasa; Ueyama Yoshito; Tamaoki Norikazu; Nomura Tatsuji; Kitahara Osamu; Yanagawa Rempei; Hirata Koichi; Nakamura Yusuke

CORPORATE SOURCE: Laboratory of Molecular Medicine, Human Genome Center, Institute of Medical Science, The University of Tokyo, Tokyo 108-8639, Japan.

SOURCE: CANCER RESEARCH, (2002 Jan 15) 62 (2) 518-27.
Journal code: 2984705R. ISSN: 0008-5472.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200202

ENTRY DATE: Entered STN: 20020128
Last Updated on STN: 20020216
Entered Medline: 20020215

AB One of the most critical issues to be solved in regard to cancer

chemotherapy is the need to establish a method for predicting efficacy or toxicity of anticancer drugs for individual patients. To identify genes that might be associated with chemosensitivity, we used a cDNA **microarray** representing 23,040 genes to analyze expression profiles in a panel of 85 cancer xenografts derived from nine human organs. The xenografts, implanted into nude mice, were examined for sensitivity to nine anticancer drugs (5-fluorouracil, 3-[(4-amino-2-methyl-5-pyrimidinyl)methyl]-1-(2-chloroethyl)-1-nitrosourea hydrochloride, adriamycin, cyclophosphamide, cisplatin, mitomycin C, methotrexate, vincristine, and vinblastine). Comparison of the **gene expression** profiles of the tumors with sensitivities to each drug identified 1,578 genes whose expression levels correlated significantly with chemosensitivity; 333 of those genes showed significant correlation with two or more drugs, and 32 correlated with six or seven drugs. These data should contribute useful information for identifying predictive markers for drug sensitivity that may eventually provide "personalized chemotherapy" for individual patients, as well as for development of novel drugs to overcome acquired resistance of tumor cells to chemical agents.

L10 ANSWER 7 OF 80 MEDLINE
ACCESSION NUMBER: 2002091288 MEDLINE
DOCUMENT NUMBER: 21679760 PubMed ID: 11821959
TITLE: Global **gene expression** profiling in Barrett's esophagus and esophageal cancer: a comparative analysis using cDNA microarrays.
AUTHOR: Selaru F M; Zou T; Xu Y; Shustova V; Yin J; Mori Y; Sato F; Wang S; Olaru A; Shibata D; Greenwald B D; Krasna M J; Abraham J M; Meltzer S J
CORPORATE SOURCE: Department of Medicine, Division of Gastroenterology, Greenebaum Cancer Center, University of Maryland School of Medicine, Baltimore VA Hospital, MD 21201, USA.
CONTRACT NUMBER: CA77057 (NCI)
CA85069 (NCI)
CA95323 (NCI)
DK47717 (NIDDK)
SOURCE: ONCOGENE, (2002 Jan 17) 21 (3) 475-8.
Journal code: 8711562. ISSN: 0950-9232.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20020201
Last Updated on STN: 20020215
Entered Medline: 20020214

AB In order to identify and contrast global **gene expression** profiles defining the premalignant syndrome, Barrett's esophagus, as well as frank esophageal cancer, we utilized cDNA **microarray** technology in conjunction with bioinformatics tools. We hybridized microarrays, each containing 8000 cDNA clones, to RNAs extracted from 13 esophageal surgical or endoscopic biopsy specimens (seven Barrett's metaplasias and six esophageal carcinomas). Hierarchical **cluster analysis** was performed on these results and displayed using a color-coded graphic representation (Treeview). The esophageal samples clustered naturally into two principal groups, each possessing unique global **gene expression** profiles. After retrieving histologic reports for these tissues, we found that one main cluster contained all seven Barrett's samples, while the remaining principal cluster comprised the six esophageal cancers. The cancers also clustered according to histopathological subtype. Thus, squamous cell carcinomas (SCCAs) constituted one group, adenocarcinomas (ADCAs) clustered separately, and one signet-ring carcinoma was in its own cluster, distinct from the ADCA cluster. We conclude that cDNA microarrays and bioinformatics show promise in the classification of esophageal malignant

and premalignant diseases, and that these methods can be applied to small biopsy samples.

L10 ANSWER 8 OF 80 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2002225478 IN-PROCESS
DOCUMENT NUMBER: 21959637 PubMed ID: 11960622
TITLE: **Microarray** detection of **gene expression** changes induced by 1,25(OH)(2)D(3) and a Ca(2+) influx-activating analog in osteoblastic ROS 17/2.8 cells.
AUTHOR: Farach-Carson Mary C; Xu Yihuan
CORPORATE SOURCE: Department of Biological Sciences, 51 E. Main Street, University of Delaware, 19716, Newark, DE, USA.
SOURCE: STEROIDS, (2002 May) 67 (6) 467-70.
Journal code: 0404536. ISSN: 0039-128X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020419
Last Updated on STN: 20020419

AB 1,25-Dihydroxyvitamin D(3) (1,25(OH)(2)D(3)) treatment of osteoblastic ROS 17/2.8 cells initiates membrane-initiated rapid responses through activation of Ca(2+) influx and longer-term nuclear receptor-mediated changes in **gene expression**. Ca(2+) influx triggers a change in the phosphorylation state of the bone matrix protein, osteopontin (OPN), detectable at 3 h and prior to nuclear receptor-mediated events. This study aimed to determine if Ca(2+) influx induced by 1,25(OH)(2)D(3) would produce nuclear receptor-independent changes in **gene expression**. We employed a rat cDNA **microarray** strategy to screen the transcriptional changes at 3 h of treatment with 1,25(OH)(2)D(3) and with an analog of 1,25(OH)(2)D(3) (25(OH)-16ene-23yne-D(3) [AT]) that we previously showed to activate Ca(2+) influx without binding to the nuclear receptor. Arrays also were screened with cDNA from ROS 17/2.8 cells treated for 24 h, when nuclear receptor-mediated transcriptional events would occur. Rat gene filters (GeneFilter, Research Genetics) were hybridized with labeled cDNA probes from treatment groups. Among 5000 different clones on the **array** filters, we identified a family of genes which were altered 2-fold or greater following treatment with 1,25(OH)(2)D(3) or analog AT for 3 h. **Cluster analysis** also revealed genes whose expression was significantly up-regulated at 24 h, including OPN. Analysis of rapid changes in **gene expression** revealed changes affecting a diverse range of cellular pathways and functions, including protein kinases and phosphatases, Ca(2+) signaling, cell adhesion and secretion. These findings provide clear evidence of rapid changes in **gene expression** associated with Ca(2+) influx mediated by 1,25(OH)(2)D(3), and shed light on the nuclear-receptor independent signaling pathway affecting OPN phosphorylation.

L10 ANSWER 9 OF 80 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2002159638 MEDLINE
DOCUMENT NUMBER: 21888419 PubMed ID: 11890715
TITLE: Expression of cytokine- and chemokine-related genes in peripheral blood mononuclear cells from lupus patients by cDNA **array**.
AUTHOR: Rus Violeta; Atamas Sergei P; Shustova Valentina; Luzina Irina G; Selaru Florin; Magder Laurence S; Via Charles S
CORPORATE SOURCE: Division of Rheumatology and Clinical Immunology, Department of Medicine, University of Maryland Medical School, Baltimore, Maryland 21201, USA.. vrus@umaryland.edu
CONTRACT NUMBER: 1 K23 AR02135-01A1 (NIAMS)
1R03AR47110 (NIAMS)
SOURCE: CLINICAL IMMUNOLOGY, (2002 Mar) 102 (3) 283-90.

Journal code: 100883537. ISSN: 1521-6616.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020314
Last Updated on STN: 20020418
Entered Medline: 20020417

AB Systemic lupus erythematosus (SLE) is characterized by diverse and complex immune abnormalities. In an effort to begin to characterize the full complexity of immune abnormalities, the expression pattern of 375 potentially relevant genes was analyzed using peripheral blood mononuclear cells (PBMC) from 21 SLE patients and 12 controls by cDNA arrays. When mean **gene expression** for patients was compared to controls, 50 genes were identified that exhibited more than 2.5-fold difference in expression level. By the Mann-Whitney U test, 20 genes were significantly different ($P < 0.05$) between patients and controls. Most of these genes have not been previously associated with SLE and belong to a variety of families such as TNF/death receptor, IL-1 cytokine family, and IL-8 and its receptors. Hierarchical clustering of samples and differentially expressed genes revealed that with few exceptions, patients clustered separately from controls. These results highlight the potential use of the **microarray** data in identifying genes associated with SLE, which could become candidate molecular markers or future therapeutic targets.

L10 ANSWER 10 OF 80 MEDLINE
ACCESSION NUMBER: 2002086022 MEDLINE
DOCUMENT NUMBER: 21642071 PubMed ID: 11782383
TITLE: Global **gene expression** analysis of gastric cancer by oligonucleotide microarrays.
AUTHOR: Hippo Yoshitaka; Taniguchi Hirokazu; Tsutsumi Shuichi; Machida Naoko; Chong Ja-Mun; Fukayama Masashi; Kodama Tatsuhiko; Aburatani Hiroyuki
CORPORATE SOURCE: Genome Science Division, The University of Tokyo, Tokyo 153-8904, Japan.
SOURCE: CANCER RESEARCH, (2002 Jan 1) 62 (1) 233-40.
Journal code: 2984705R. ISSN: 0008-5472.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20020130
Last Updated on STN: 20020213
Entered Medline: 20020212

AB To gain molecular understanding of carcinogenesis, progression, and diversity of gastric cancer, 22 primary human advanced gastric cancer tissues and 8 noncancerous gastric tissues were analyzed by high-density oligonucleotide **microarray** in this study. Based on expression analysis of approximately 6800 genes, a two-way clustering algorithm successfully distinguished cancer tissues from noncancerous tissues. Subsequently, genes that were differentially expressed in cancer and noncancerous tissues were identified; 162 and 129 genes were highly expressed ($P < 0.05$) >2.5-fold in cancer tissues and noncancerous tissues, respectively. In cancer tissues, genes related to cell cycle, growth factor, cell motility, cell adhesion, and matrix remodeling were highly expressed. In noncancerous tissues, genes related to gastrointestinal-specific function and immune response were highly expressed. Furthermore, we identified several genes associated with lymph node metastasis including Oct-2 or histological types including Liver-Intestine Cadherin. These results provide not only a new molecular basis for understanding biological properties of gastric cancer, but also useful resources for

future development of therapeutic targets and diagnostic markers for gastric cancer.

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 NEWS  1           Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2  Jan 25   BLAST(R) searching in REGISTRY available in STN on the Web
 NEWS  3  Jan 29   FSTA has been reloaded and moves to weekly updates
 NEWS  4  Feb 01   DKILIT now produced by FIZ Karlsruhe and has a new update
                   frequency
 NEWS  5  Feb 19   Access via Tymnet and SprintNet Eliminated Effective 3/31/02
 NEWS  6  Mar 08   Gene Names now available in BIOSIS
 NEWS  7  Mar 22   TOXLIT no longer available
 NEWS  8  Mar 22   TRCTHERMO no longer available
 NEWS  9  Mar 28   US Provisional Priorities searched with P in CA/CAplus
                   and USPATFULL
 NEWS 10  Mar 28   LIPINSKI/CALC added for property searching in REGISTRY
 NEWS 11  Apr 02   PAPERCHEM no longer available on STN.  Use PAPERCHEM2 instead.
 NEWS 12  Apr 08   "Ask CAS" for self-help around the clock
 NEWS 13  Apr 09   BEILSTEIN: Reload and Implementation of a New Subject Area
 NEWS 14  Apr 09   ZDB will be removed from STN
 NEWS 15  Apr 19   US Patent Applications available in IFICDB, IFIPAT, and IFIUDB
 NEWS 16  Apr 22   Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
 NEWS 17  Apr 22   BIOSIS Gene Names now available in TOXCENTER
 NEWS 18  Apr 22   Federal Research in Progress (FEDRIP) now available

 NEWS EXPRESS  February 1 CURRENT WINDOWS VERSION IS V6.0d,
               CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP),
               AND CURRENT DISCOVER FILE IS DATED 05 FEBRUARY 2002
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=> s gene expression
   4 FILES SEARCHED...
L1      700092 GENE EXPRESSION

=> s cluster analysis
L2       21071 CLUSTER ANALYSIS

=> s l1 and l2
L3         577 L1 AND L2

=> array
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=> s array
L4      129141 ARRAY

=> s l3 and l4
L5         183 L3 AND L4

=> s microarray
L6       12481 MICROARRAY

=> s l5 and l6
L7          95 L5 AND L6

=> sl7 not p7>1999
SL7 IS NOT A RECOGNIZED COMMAND
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"HELP COMMANDS" at an arrow prompt (=>).

=> s l7 not py>1999
L8           0 L7 NOT PY>1999

=> s l7 not py>1998
L9           0 L7 NOT PY>1998

=> dup rem l7
PROCESSING COMPLETED FOR L7
L10          80 DUP REM L7 (15 DUPLICATES REMOVED)

=> d ti l10 1-30
```

L10 ANSWER 1 OF 80 MEDLINE
TI Differential gene regulation by the two progesterone receptor isoforms in human breast cancer cells.

L10 ANSWER 2 OF 80 MEDLINE
TI DNA **microarray** analysis of differential **gene expression** in Borrelia burgdorferi, the Lyme disease spirochete.

L10 ANSWER 3 OF 80 MEDLINE
TI Identifying pre-post chemotherapy differences in **gene expression** in breast tumours: a statistical method appropriate for this aim.

L10 ANSWER 4 OF 80 MEDLINE DUPLICATE 1
TI High-density **microarray** analysis of hippocampal **gene expression** following experimental brain injury.

L10 ANSWER 5 OF 80 MEDLINE
TI **Gene expression** profiling predicts clinical outcome of breast cancer.

L10 ANSWER 6 OF 80 MEDLINE
TI Genome-wide cDNA **microarray** screening to correlate **gene expression** profiles with sensitivity of 85 human cancer xenografts to anticancer drugs.

L10 ANSWER 7 OF 80 MEDLINE
TI Global **gene expression** profiling in Barrett's esophagus and esophageal cancer: a comparative analysis using cDNA microarrays.

L10 ANSWER 8 OF 80 MEDLINE DUPLICATE 2
TI **Microarray** detection of **gene expression** changes induced by 1,25(OH)(2)D(3) and a Ca(2+) influx-activating analog in osteoblastic ROS 17/2.8 cells.

L10 ANSWER 9 OF 80 MEDLINE DUPLICATE 3
TI Expression of cytokine- and chemokine-related genes in peripheral blood mononuclear cells from lupus patients by cDNA **array**.

L10 ANSWER 10 OF 80 MEDLINE
TI Global **gene expression** analysis of gastric cancer by oligonucleotide microarrays.

L10 ANSWER 11 OF 80 MEDLINE
TI The advantages of cDNA **microarray** as an effective tool for identification of reproductive organ-specific genes in a model legume, Lotus japonicus.

L10 ANSWER 12 OF 80 MEDLINE
TI Screening of **gene expression** profiles in gastric epithelial cells induced by Helicobacter pylori using **microarray** analysis.

L10 ANSWER 13 OF 80 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Identification of genes differentially expressed in cultured human osteoblasts versus human fibroblasts by DNA **microarray** analysis.

L10 ANSWER 14 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Methods for gene profiling arrays involving RNA or cDNA amplification

L10 ANSWER 15 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Method for selecting differentially expressed genes for use in informative nucleic acid arrays

L10 ANSWER 16 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Methods for **gene expression** profiling to diagnose disease, monitor drug therapy, identify physiological states, and identify differentially expressed genes in secretory versus proliferative endometrium

L10 ANSWER 17 OF 80 MEDLINE DUPLICATE 4
TI Bootstrapping **cluster analysis**: assessing the reliability of conclusions from **microarray** experiments.

L10 ANSWER 18 OF 80 MEDLINE
TI The consequences of chromosomal aneuploidy on **gene expression** profiles in a cell line model for prostate carcinogenesis.

L10 ANSWER 19 OF 80 MEDLINE
TI Estrogen receptor status in breast cancer is associated with remarkably distinct **gene expression** patterns.

L10 ANSWER 20 OF 80 MEDLINE DUPLICATE 5
TI Molecular profiling of transformed and metastatic murine squamous carcinoma cells by differential display and cDNA **microarray** reveals altered expression of multiple genes related to growth, apoptosis, angiogenesis, and the NF-kappaB signal pathway.

L10 ANSWER 21 OF 80 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 6
TI Papillomavirus type 16 oncogenes downregulate expression of interferon-responsive genes and upregulate proliferation-associated and NF-.kappa.B-responsive genes in cervical keratinocytes

L10 ANSWER 22 OF 80 MEDLINE
TI DNA **microarray** analysis of genes involved in p53 mediated apoptosis: activation of Apaf-1.

L10 ANSWER 23 OF 80 MEDLINE
TI New molecular phenotypes in the dst mutants of Arabidopsis revealed by DNA **microarray** analysis.

L10 ANSWER 24 OF 80 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI High-sensitivity **array** analysis of **gene expression** for the early detection of disseminated breast tumor cells in peripheral blood.

L10 ANSWER 25 OF 80 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Identification of **gene expression** patterns in superficial and invasive human bladder cancer.

L10 ANSWER 26 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI **Gene expression** in 1-trial learning of a conditioned taste aversion.

L10 ANSWER 27 OF 80 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Distinct **gene expression** profiling in chronic lymphocytic leukemia with 11q23 deletion.

L10 ANSWER 28 OF 80 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
TI **Gene expression** profiling of B cell chronic lymphocytic leukemia reveals a homogenous phenotype related to memory B cells;
cluster analysis, DNA chip, and DNA **microarray**

L10 ANSWER 29 OF 80 CAPLUS COPYRIGHT 2002 ACS

TI Establishment of normal, terminally differentiating mouse erythroid progenitors: molecular characterization by cDNA arrays

L10 ANSWER 30 OF 80 MEDLINE
TI RNA expression in the early characterization of hepatotoxicants in Wistar rats by high-density DNA microarrays.

=> d ibib abs l10 1-10

L10 ANSWER 1 OF 80 MEDLINE
ACCESSION NUMBER: 2002106152 MEDLINE
DOCUMENT NUMBER: 21826375 PubMed ID: 11717311
TITLE: Differential gene regulation by the two progesterone receptor isoforms in human breast cancer cells.
AUTHOR: Richer Jennifer K; Jacobsen Britta M; Manning Nicole G; Abel M Greg; Wolf Douglas M; Horwitz Kathryn B
CORPORATE SOURCE: Department of Medicine/Endocrinology, University of Colorado School of Medicine, Denver, Colorado 80262, USA.. jennifer.richer@uchsc.edu
CONTRACT NUMBER: CA26869 (NCI)
DK48238 (NIDDK)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2002 Feb 15) 277 (7) 5209-18.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200203
ENTRY DATE: Entered STN: 20020212
Last Updated on STN: 20020322
Entered Medline: 20020321
AB The PR-A and PR-B isoforms of progesterone receptors (PR) have different physiological functions, and their ratio varies widely in breast cancers. To determine whether the two PR regulate different genes, we used human breast cancer cell lines engineered to express one or the other isoform. Cells were treated with progesterone in triplicate, time-separated experiments, allowing statistical analyses of **microarray gene expression** data. Of 94 progesterone-regulated genes, 65 are uniquely regulated by PR-B, 4 uniquely by PR-A, and only 25 by both. Almost half the genes encode proteins that are membrane-bound or involved in membrane-initiated signaling. We also find an important set of progesterone-regulated genes involved in mammary gland development and/or implicated in breast cancer. This first, large scale study of PR gene regulation has important implications for the measurement of PR in breast cancers and for the many clinical uses of synthetic progestins. It suggests that it is important to distinguish between the two isoforms in breast cancers and that isoform-specific genes can be used to screen for ligands that selectively modulate the activity of PR-A or PR-B. Additionally, use of natural target genes, rather than "consensus" response elements, for transcription studies should improve our understanding of steroid hormone action.

L10 ANSWER 2 OF 80 MEDLINE
ACCESSION NUMBER: 2002111052 MEDLINE
DOCUMENT NUMBER: 21819468 PubMed ID: 11830671
TITLE: DNA **microarray** analysis of differential **gene expression** in Borrelia burgdorferi, the Lyme disease spirochete.
AUTHOR: Revel Andrew T; Talaat Adel M; Norgard Michael V
CORPORATE SOURCE: Department of Microbiology, University of Texas Southwestern Medical Center, Dallas, TX 75390, USA.
CONTRACT NUMBER: AI-45538 (NIAID)

SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2002 Feb 5) 99 (3) 1562-7. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200203
ENTRY DATE: Entered STN: 20020215
Last Updated on STN: 20020308
Entered Medline: 20020307

AB DNA microarrays were used to survey the adaptive genetic responses of Borrelia burgdorferi (Bb) B31, the Lyme disease spirochete, when grown under conditions analogous to those found in unfed ticks (UTs), fed ticks (FTs), or during mammalian host adaptation (Bb in dialysis membrane chambers implanted in rats). Microarrays contained 95.4% of the predicted B31 genes, 150 (8.6%) of which were differentially regulated (changes of > or = 1.8-fold) among the three growth conditions. A substantial proportion (46%) of the differentially regulated genes encoded proteins with predicted export signals (29% from predicted lipoproteins), emphasizing the importance to Bb of modulating its extracellular proteome. For B31 cultivated at the more restrictive UT condition, **microarray** data provided evidence of a bacterial stringent response and factors that restrict cell division. A large proportion of genes were responsive to the FT growth condition, wherein increased temperature and reduced pH were prominent environmental parameters. A surprising theme, supported by **cluster analysis**, was that many of the **gene expression** changes induced during the FT growth condition were transient and largely tempered as B31 adapted to the mammalian host, suggesting that once Bb gains entry and adapts to mammalian tissues, fewer differentially regulated genes are exploited. It therefore would seem that although widely dissimilar, the UT and dialysis membrane chamber growth conditions promote more static patterns of **gene expression** in Bb. The **microarray** data thus provide a basis for formulating new testable hypotheses regarding the life cycle of Bb and attaining a more complete understanding of many aspects of Bb's complex parasitic strategies.

L10 ANSWER 3 OF 80 MEDLINE
ACCESSION NUMBER: 2002216642 MEDLINE
DOCUMENT NUMBER: 21949770 PubMed ID: 11953855
TITLE: Identifying pre-post chemotherapy differences in **gene expression** in breast tumours: a statistical method appropriate for this aim.
AUTHOR: Korn E L; McShane L M; Troendle J F; Rosenwald A; Simon R
CORPORATE SOURCE: Biometric Research Branch, EPN-8128, National Cancer Institute, National Institutes of Health, Bethesda MD 20892, USA.. korne@ctep.nci.nih.gov
SOURCE: BRITISH JOURNAL OF CANCER, (2002 Apr 8) 86 (7) 1093-6. Journal code: 0370635. ISSN: 0007-0920.
PUB. COUNTRY: Scotland: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020416
Last Updated on STN: 20020501
Entered Medline: 20020430

AB Although widely used for the analysis of **gene expression** **microarray** data, **cluster analysis** may not be the most appropriate statistical technique for some study aims. We demonstrate this by considering a previous analysis of **microarray** data obtained on breast tumour specimens, many of which were paired specimens from the same patient before and after chemotherapy. Reanalysing

the data using statistical methods that appropriately utilise the paired differences for identification of differentially expressed genes, we find 17 genes that we can confidently identify as more expressed after chemotherapy than before. These findings were not reported by the original investigators who analysed the data using **cluster analysis** techniques.

L10 ANSWER 4 OF 80 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2002159238 MEDLINE
DOCUMENT NUMBER: 21888965 PubMed ID: 11891777
TITLE: High-density **microarray** analysis of hippocampal **gene expression** following experimental brain injury.
AUTHOR: Matzilevich David A; Rall Jason M; Moore Anthony N; Grill Raymond J; Dash Pramod K
CORPORATE SOURCE: The Vivian L. Smith Center for Neurologic Research, Departments of Neurobiology and Anatomy, Neurosurgery, The University of Texas Medical School, Houston, Texas 77225, USA.
CONTRACT NUMBER: MH49662 (NIMH)
NS3545 (NINDS)
P50NS23327 (NINDS)
SOURCE: JOURNAL OF NEUROSCIENCE RESEARCH, (2002 Mar 1) 67 (5) 646-63.
Journal code: 7600111. ISSN: 0360-4012.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020314
Last Updated on STN: 20020501
Entered Medline: 20020430
AB Behavioral, biophysical, and pharmacological studies have implicated the hippocampus in the formation and storage of spatial memory. Traumatic brain injury (TBI) often causes spatial memory deficits, which are thought to arise from the death as well as the dysfunction of hippocampal neurons. Cell death and dysfunction are commonly associated with and often caused by altered expression of specific genes. The identification of the genes involved in these processes, as well as those participating in postinjury cellular repair and plasticity, is important for the development of mechanism-based therapies. To monitor the expression levels of a large number of genes and to identify genes not previously implicated in TBI pathophysiology, a high-density oligonucleotide **array** containing 8,800 genes was interrogated. RNA samples were prepared from ipsilateral hippocampi 3 hr and 24 hr following lateral cortical impact injury and compared to samples from sham-operated controls. **Cluster analysis** was employed using statistical algorithms to arrange the genes according to similarity in patterns of expression. The study indicates that the genomic response to TBI is complex, affecting approximately 6% (at the time points examined) of the total number of genes examined. The identity of the genes revealed that TBI affects many aspects of cell physiology, including oxidative stress, metabolism, inflammation, structural changes, and cellular signaling. The analysis revealed genes whose expression levels have been reported to be altered in response to injury as well as several genes not previously implicated in TBI pathophysiology.

L10 ANSWER 5 OF 80 MEDLINE
ACCESSION NUMBER: 2002099463 MEDLINE
DOCUMENT NUMBER: 21681887 PubMed ID: 11823860
TITLE: **Gene expression** profiling predicts clinical outcome of breast cancer.
COMMENT: Comment in: Nature. 2002 Jan 31;415(6871):484-5

AUTHOR: van 't Veer Laura J; Dai Hongyue; van de Vijver Marc J; He Yudong D; Hart Augustinus A M; Mao Mao; Peterse Hans L; van der Kooy Karin; Marton Matthew J; Witteveen Anke T; Schreiber George J; Kerkhoven Ron M; Roberts Chris; Linsley Peter S; Bernards Rene; Friend Stephen H

CORPORATE SOURCE: Division of Diagnostic Oncology, The Netherlands Cancer Institute, 121 Plesmanlaan, 1066 CX Amsterdam, The Netherlands.

SOURCE: NATURE, (2002 Jan 31) 415 (6871) 530-6.
Journal code: 0410462. ISSN: 0028-0836.

PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200203

ENTRY DATE: Entered STN: 20020207
Last Updated on STN: 20020313
Entered Medline: 20020312

AB Breast cancer patients with the same stage of disease can have markedly different treatment responses and overall outcome. The strongest predictors for metastases (for example, lymph node status and histological grade) fail to classify accurately breast tumours according to their clinical behaviour. Chemotherapy or hormonal therapy reduces the risk of distant metastases by approximately one-third; however, 70-80% of patients receiving this treatment would have survived without it. None of the signatures of breast cancer **gene expression** reported to date allow for patient-tailored therapy strategies. Here we used DNA **microarray** analysis on primary breast tumours of 117 young patients, and applied supervised classification to identify a **gene expression** signature strongly predictive of a short interval to distant metastases ('poor prognosis' signature) in patients without tumour cells in local lymph nodes at diagnosis (lymph node negative). In addition, we established a signature that identifies tumours of BRCA1 carriers. The poor prognosis signature consists of genes regulating cell cycle, invasion, metastasis and angiogenesis. This **gene expression** profile will outperform all currently used clinical parameters in predicting disease outcome. Our findings provide a strategy to select patients who would benefit from adjuvant therapy.

L10 ANSWER 6 OF 80 MEDLINE

ACCESSION NUMBER: 2002082994 MEDLINE

DOCUMENT NUMBER: 21668025 PubMed ID: 11809704

TITLE: Genome-wide cDNA **microarray** screening to correlate **gene expression** profiles with sensitivity of 85 human cancer xenografts to anticancer drugs.

AUTHOR: Zembutsu Hitoshi; Ohnishi Yasuyuki; Tsunoda Tatsuhiko; Furukawa Yoichi; Katagiri Toyomasa; Ueyama Yoshito; Tamaoki Norikazu; Nomura Tatsuji; Kitahara Osamu; Yanagawa Rempei; Hirata Koichi; Nakamura Yusuke

CORPORATE SOURCE: Laboratory of Molecular Medicine, Human Genome Center, Institute of Medical Science, The University of Tokyo, Tokyo 108-8639, Japan.

SOURCE: CANCER RESEARCH, (2002 Jan 15) 62 (2) 518-27.
Journal code: 2984705R. ISSN: 0008-5472.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200202

ENTRY DATE: Entered STN: 20020128
Last Updated on STN: 20020216
Entered Medline: 20020215

AB One of the most critical issues to be solved in regard to cancer

chemotherapy is the need to establish a method for predicting efficacy or toxicity of anticancer drugs for individual patients. To identify genes that might be associated with chemosensitivity, we used a cDNA **microarray** representing 23,040 genes to analyze expression profiles in a panel of 85 cancer xenografts derived from nine human organs. The xenografts, implanted into nude mice, were examined for sensitivity to nine anticancer drugs (5-fluorouracil, 3-[(4-amino-2-methyl-5-pyrimidinyl)methyl]-1-(2-chloroethyl)-1-nitrosourea hydrochloride, adriamycin, cyclophosphamide, cisplatin, mitomycin C, methotrexate, vincristine, and vinblastine). Comparison of the **gene expression** profiles of the tumors with sensitivities to each drug identified 1,578 genes whose expression levels correlated significantly with chemosensitivity; 333 of those genes showed significant correlation with two or more drugs, and 32 correlated with six or seven drugs. These data should contribute useful information for identifying predictive markers for drug sensitivity that may eventually provide "personalized chemotherapy" for individual patients, as well as for development of novel drugs to overcome acquired resistance of tumor cells to chemical agents.

L10 ANSWER 7 OF 80 MEDLINE
ACCESSION NUMBER: 2002091288 MEDLINE
DOCUMENT NUMBER: 21679760 PubMed ID: 11821959
TITLE: Global **gene expression** profiling in Barrett's esophagus and esophageal cancer: a comparative analysis using cDNA microarrays.
AUTHOR: Selaru F M; Zou T; Xu Y; Shustova V; Yin J; Mori Y; Sato F; Wang S; Olaru A; Shibata D; Greenwald B D; Krasna M J; Abraham J M; Meltzer S J
CORPORATE SOURCE: Department of Medicine, Division of Gastroenterology, Greenebaum Cancer Center, University of Maryland School of Medicine, Baltimore VA Hospital, MD 21201, USA.
CONTRACT NUMBER: CA77057 (NCI)
CA85069 (NCI)
CA95323 (NCI)
DK47717 (NIDDK)
SOURCE: ONCOGENE, (2002 Jan 17) 21 (3) 475-8.
Journal code: 8711562. ISSN: 0950-9232.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20020201
Last Updated on STN: 20020215
Entered Medline: 20020214

AB In order to identify and contrast global **gene expression** profiles defining the premalignant syndrome, Barrett's esophagus, as well as frank esophageal cancer, we utilized cDNA **microarray** technology in conjunction with bioinformatics tools. We hybridized microarrays, each containing 8000 cDNA clones, to RNAs extracted from 13 esophageal surgical or endoscopic biopsy specimens (seven Barrett's metaplasias and six esophageal carcinomas). Hierarchical **cluster analysis** was performed on these results and displayed using a color-coded graphic representation (Treeview). The esophageal samples clustered naturally into two principal groups, each possessing unique global **gene expression** profiles. After retrieving histologic reports for these tissues, we found that one main cluster contained all seven Barrett's samples, while the remaining principal cluster comprised the six esophageal cancers. The cancers also clustered according to histopathological subtype. Thus, squamous cell carcinomas (SCCAs) constituted one group, adenocarcinomas (ADCAs) clustered separately, and one signet-ring carcinoma was in its own cluster, distinct from the ADCA cluster. We conclude that cDNA microarrays and bioinformatics show promise in the classification of esophageal malignant

and premalignant diseases, and that these methods can be applied to small biopsy samples.

L10 ANSWER 8 OF 80 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2002225478 IN-PROCESS
DOCUMENT NUMBER: 21959637 PubMed ID: 11960622
TITLE: **Microarray** detection of **gene expression** changes induced by 1,25(OH)(2)D(3) and a Ca(2+) influx-activating analog in osteoblastic ROS 17/2.8 cells.
AUTHOR: Farach-Carson Mary C; Xu Yihuan
CORPORATE SOURCE: Department of Biological Sciences, 51 E. Main Street, University of Delaware, 19716, Newark, DE, USA.
SOURCE: STEROIDS, (2002 May) 67 (6) 467-70.
Journal code: 0404536. ISSN: 0039-128X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020419
Last Updated on STN: 20020419
AB 1,25-Dihydroxyvitamin D(3) (1,25(OH)(2)D(3)) treatment of osteoblastic ROS 17/2.8 cells initiates membrane-initiated rapid responses through activation of Ca(2+) influx and longer-term nuclear receptor-mediated changes in **gene expression**. Ca(2+) influx triggers a change in the phosphorylation state of the bone matrix protein, osteopontin (OPN), detectable at 3 h and prior to nuclear receptor-mediated events. This study aimed to determine if Ca(2+) influx induced by 1,25(OH)(2)D(3) would produce nuclear receptor-independent changes in **gene expression**. We employed a rat cDNA **microarray** strategy to screen the transcriptional changes at 3 h of treatment with 1,25(OH)(2)D(3) and with an analog of 1,25(OH)(2)D(3) (25(OH)-16ene-23yne-D(3) [AT]) that we previously showed to activate Ca(2+) influx without binding to the nuclear receptor. Arrays also were screened with cDNA from ROS 17/2.8 cells treated for 24 h, when nuclear receptor-mediated transcriptional events would occur. Rat gene filters (GeneFilter, Research Genetics) were hybridized with labeled cDNA probes from treatment groups. Among 5000 different clones on the **array** filters, we identified a family of genes which were altered 2-fold or greater following treatment with 1,25(OH)(2)D(3) or analog AT for 3 h. **Cluster analysis** also revealed genes whose expression was significantly up-regulated at 24 h, including OPN. Analysis of rapid changes in **gene expression** revealed changes affecting a diverse range of cellular pathways and functions, including protein kinases and phosphatases, Ca(2+) signaling, cell adhesion and secretion. These findings provide clear evidence of rapid changes in **gene expression** associated with Ca(2+) influx mediated by 1,25(OH)(2)D(3), and shed light on the nuclear-receptor independent signaling pathway affecting OPN phosphorylation.

L10 ANSWER 9 OF 80 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2002159638 MEDLINE
DOCUMENT NUMBER: 21888419 PubMed ID: 11890715
TITLE: Expression of cytokine- and chemokine-related genes in peripheral blood mononuclear cells from lupus patients by cDNA **array**.
AUTHOR: Rus Violeta; Atamas Sergei P; Shustova Valentina; Luzina Irina G; Selaru Florin; Magder Laurence S; Via Charles S
CORPORATE SOURCE: Division of Rheumatology and Clinical Immunology, Department of Medicine, University of Maryland Medical School, Baltimore, Maryland 21201, USA.. vrus@umaryland.edu
CONTRACT NUMBER: 1 K23 AR02135-01A1 (NIAMS)
1R03AR47110 (NIAMS)
SOURCE: CLINICAL IMMUNOLOGY, (2002 Mar) 102 (3) 283-90.

Journal code: 100883537. ISSN: 1521-6616.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020314
Last Updated on STN: 20020418
Entered Medline: 20020417

AB Systemic lupus erythematosus (SLE) is characterized by diverse and complex immune abnormalities. In an effort to begin to characterize the full complexity of immune abnormalities, the expression pattern of 375 potentially relevant genes was analyzed using peripheral blood mononuclear cells (PBMC) from 21 SLE patients and 12 controls by cDNA arrays. When mean **gene expression** for patients was compared to controls, 50 genes were identified that exhibited more than 2.5-fold difference in expression level. By the Mann-Whitney U test, 20 genes were significantly different ($P < 0.05$) between patients and controls. Most of these genes have not been previously associated with SLE and belong to a variety of families such as TNF/death receptor, IL-1 cytokine family, and IL-8 and its receptors. Hierarchical clustering of samples and differentially expressed genes revealed that with few exceptions, patients clustered separately from controls. These results highlight the potential use of the **microarray** data in identifying genes associated with SLE, which could become candidate molecular markers or future therapeutic targets.

L10 ANSWER 10 OF 80 MEDLINE
ACCESSION NUMBER: 2002086022 MEDLINE
DOCUMENT NUMBER: 21642071 PubMed ID: 11782383
TITLE: Global **gene expression** analysis of gastric cancer by oligonucleotide microarrays.
AUTHOR: Hippo Yoshitaka; Taniguchi Hirokazu; Tsutsumi Shuichi; Machida Naoko; Chong Ja-Mun; Fukayama Masashi; Kodama Tatsuhiko; Aburatani Hiroyuki
CORPORATE SOURCE: Genome Science Division, The University of Tokyo, Tokyo 153-8904, Japan.
SOURCE: CANCER RESEARCH, (2002 Jan 1) 62 (1) 233-40.
Journal code: 2984705R. ISSN: 0008-5472.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20020130
Last Updated on STN: 20020213
Entered Medline: 20020212

AB To gain molecular understanding of carcinogenesis, progression, and diversity of gastric cancer, 22 primary human advanced gastric cancer tissues and 8 noncancerous gastric tissues were analyzed by high-density oligonucleotide **microarray** in this study. Based on expression analysis of approximately 6800 genes, a two-way clustering algorithm successfully distinguished cancer tissues from noncancerous tissues. Subsequently, genes that were differentially expressed in cancer and noncancerous tissues were identified; 162 and 129 genes were highly expressed ($P < 0.05$) >2.5-fold in cancer tissues and noncancerous tissues, respectively. In cancer tissues, genes related to cell cycle, growth factor, cell motility, cell adhesion, and matrix remodeling were highly expressed. In noncancerous tissues, genes related to gastrointestinal-specific function and immune response were highly expressed. Furthermore, we identified several genes associated with lymph node metastasis including Oct-2 or histological types including Liver-Intestine Cadherin. These results provide not only a new molecular basis for understanding biological properties of gastric cancer, but also useful resources for

future development of therapeutic targets and diagnostic markers for gastric cancer.

=> d his

(FILE 'HOME' ENTERED AT 15:41:16 ON 09 MAY 2002)

FILE 'MEDLINE, BIOSIS, BIOTECHDS, CAPLUS, EMBASE' ENTERED AT 15:41:24 ON 09 MAY 2002

```
L1        700092 S GENE EXPRESSION
L2         21071 S CLUSTER ANALYSIS
L3           577 S L1 AND L2
L4        129141 S ARRAY
L5           183 S L3 AND L4
L6         12481 S MICROARRAY
L7            95 S L5 AND L6
L8             0 S L7 NOT PY>1999
L9             0 S L7 NOT PY>1998
L10           80 DUP REM L7 (15 DUPLICATES REMOVED)

=> dup rem l10
PROCESSING COMPLETED FOR L10
L11           80 DUP REM L10 (0 DUPLICATES REMOVED)

=> s l11 not py>2000
L12           12 L11 NOT PY>2000

=> d ti l12

L12  ANSWER 1 OF 12     MEDLINE
TI   Assessing reliability of gene clusters from gene
     expression data.
```

=> d ibib abs l12 1-12

```
L12  ANSWER 1 OF 12     MEDLINE
ACCESSION NUMBER:   2002065931     MEDLINE
DOCUMENT NUMBER:    21652689   PubMed ID: 11793234
TITLE:              Assessing reliability of gene clusters from gene
                    expression data.
AUTHOR:             Zhang K; Zhao H
CORPORATE SOURCE:   Department of Epidemiology and Public Health, Yale
                    University School of Medicine, New Haven, CT 06520, USA.
CONTRACT NUMBER:    HD36834 (NICHD)
                    MG59507
SOURCE:             Funct Integr Genomics, (2000 Nov) 1 (3) 156-73.
                    Journal code: 100939343. ISSN: 1438-793X.
PUB. COUNTRY:       Germany: Germany, Federal Republic of
                    Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        200203
ENTRY DATE:         Entered STN: 20020125
                    Last Updated on STN: 20020307
                    Entered Medline: 20020305
```

AB The rapid development of **microarray** technologies has raised many challenging problems in experiment design and data analysis. Although many numerical algorithms have been successfully applied to analyze **gene expression** data, the effects of variations and uncertainties in measured **gene expression** levels across samples and experiments have been largely ignored in the literature. In this article, in the context of hierarchical clustering

algorithms, we introduce a statistical resampling method to assess the reliability of gene clusters identified from any hierarchical clustering method. Using the clustering trees constructed from the resampled data, we can evaluate the confidence value for each node in the observed clustering tree. A majority-rule consensus tree can be obtained, showing clusters that only occur in a majority of the resampled trees. We illustrate our proposed methods with applications to two published data sets. Although the methods are discussed in the context of hierarchical clustering methods, they can be applied with other cluster-identification methods for **gene expression** data to assess the reliability of any gene cluster of interest.

L12 ANSWER 2 OF 12 MEDLINE
ACCESSION NUMBER: 2001646598 MEDLINE
DOCUMENT NUMBER: 21557040 PubMed ID: 11700594
TITLE: Cluster inference methods and graphical models evaluated on NCI60 **microarray gene expression** data.
AUTHOR: Waddell P J; Kishino H
CORPORATE SOURCE: Chugai Research Institute for Molecular Medicine, 153-2 Nagai Niihari Ibaraki 300-4101, Japan.. waddell@cimmed.com
SOURCE: GENOME INFORMATICS SERIES, (2000) 11 129-40.
Journal code: 9717234. ISSN: 0919-9454.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011112
Last Updated on STN: 20020124
Entered Medline: 20011231

AB At present, there is a lack of a sound methodology to infer causal **gene expression** relationships on a genome wide basis. We address this first by examining the behaviour of some of the latest and fastest algorithms for tree and **cluster analysis**, particularly hierarchical methods popular in phylogenetics. Combined with these are two novel distances based on partial, rather than full, correlations. Theoretically, partial correlations should provide better evidence for regulatory genetic links than standard correlations. To compare the clusters obtained by many alternative methods we use tree consensus methods. To compare methods of analysis we used tree partition metrics followed by another level of clustering. These, and a tree fit metric, all suggest that the new distances give quite different trees than those usually obtained. In the second part we consider graphical modeling of the interactions of important genes of the cell cycle. Despite the models seeming to fit well on occasions, and despite the experimental error structure seeming close to multivariate normal, there are considerable problems to overcome. Latent variables, in this case important genes missing from the analysis, are inferred to have a strong effect on the partial correlations. Also, the data show clear evidence of sampling distributions conditional on the status of important cancer related genes, including TP53. Without full information on which genes are wild type the appropriate models cannot be fitted. These findings point to the need to include and distinguish not only all relevant genes but also all splice variants in the design phase of a **microarray** analysis. Failure to do so will induce problems similar to both latent variables and conditional distributions.

L12 ANSWER 3 OF 12 MEDLINE
ACCESSION NUMBER: 2001382141 MEDLINE
DOCUMENT NUMBER: 21148270 PubMed ID: 11250685
TITLE: **Microarray** foray.
AUTHOR: Coffey R J; Threadgill D
SOURCE: Breast Cancer Res, (2000) 2 (1) 8-9. Ref: 5

Journal code: DYZ; 100927353. ISSN: 1465-5411.
PUB. COUNTRY: England: United Kingdom
Editorial
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200107
ENTRY DATE: Entered STN: 20010709
Last Updated on STN: 20010709
Entered Medline: 20010705

L12 ANSWER 4 OF 12 MEDLINE
ACCESSION NUMBER: 2001102281 MEDLINE
DOCUMENT NUMBER: 20431605 PubMed ID: 10977093
TITLE: Genes, themes and microarrays: using information retrieval for large-scale gene analysis.
AUTHOR: Shatkay H; Edwards S; Wilbur W J; Boguski M
CORPORATE SOURCE: National Center for Biotechnology Information, NLM, NIH, Bethesda, Maryland 20984, USA.. shatkay@ncbi.nlm.nih.gov
SOURCE: ISMB, (2000) 8 317-28.
Journal code: CCP.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010126

AB The immense volume of data resulting from DNA **microarray** experiments, accompanied by an increase in the number of publications discussing gene-related discoveries, presents a major data analysis challenge. Current methods for genome-wide analysis of expression data typically rely on **cluster analysis** of **gene expression** patterns. Clustering indeed reveals potentially meaningful relationships among genes, but can not explain the underlying biological mechanisms. In an attempt to address this problem, we have developed a new approach for utilizing the literature in order to establish functional relationships among genes on a genome-wide scale. Our method is based on revealing coherent themes within the literature, using a similarity-based search in document space. Content-based relationships among abstracts are then translated into functional connections among genes. We describe preliminary experiments applying our algorithm to a database of documents discussing yeast genes. A comparison of the produced results with well-established yeast gene functions demonstrates the effectiveness of our approach.

L12 ANSWER 5 OF 12 MEDLINE
ACCESSION NUMBER: 2001071436 MEDLINE
DOCUMENT NUMBER: 20553126 PubMed ID: 11101835
TITLE: The transcriptome of Arabidopsis thaliana during systemic acquired resistance.
AUTHOR: Maleck K; Levine A; Eulgem T; Morgan A; Schmid J; Lawton K A; Dangl J L; Dietrich R A
CORPORATE SOURCE: Syngenta, Research Triangle Park, North Carolina, USA.
SOURCE: NATURE GENETICS, (2000 Dec) 26 (4) 403-10.
Journal code: BRO. ISSN: 1061-4036.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322

Last Updated on STN: 20010322
Entered Medline: 20010104

AB Infected plants undergo transcriptional reprogramming during initiation of both local defence and systemic acquired resistance (SAR). We monitored **gene-expression** changes in Arabidopsis thaliana under 14 different SAR-inducing or SAR-repressing conditions using a DNA **microarray** representing approximately 25-30% of all A. thaliana genes. We derived groups of genes with common regulation patterns, or regulons. The regulon containing PR-1, a reliable marker gene for SAR in A. thaliana, contains known PR genes and novel genes likely to function during SAR and disease resistance. We identified a common promoter element in genes of this regulon that binds members of a plant-specific transcription factor family. Our results extend expression profiling to definition of regulatory networks and gene discovery in plants.

L12 ANSWER 6 OF 12 MEDLINE
ACCESSION NUMBER: 2001039008 MEDLINE
DOCUMENT NUMBER: 20504466 PubMed ID: 11035779
TITLE: Coupled two-way clustering analysis of gene **microarray** data.
AUTHOR: Getz G; Levine E; Domany E
CORPORATE SOURCE: Department of Physics of Complex Systems, Weizmann Institute of Science, Rehovot 76100, Israel.
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2000 Oct 24) 97 (22) 12079-84.
Journal code: PV3. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200011
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001128

AB We present a coupled two-way clustering approach to gene **microarray** data analysis. The main idea is to identify subsets of the genes and samples, such that when one of these is used to cluster the other, stable and significant partitions emerge. The search for such subsets is a computationally complex task. We present an algorithm, based on iterative clustering, that performs such a search. This analysis is especially suitable for gene **microarray** data, where the contributions of a variety of biological mechanisms to the **gene expression** levels are entangled in a large body of experimental data. The method was applied to two gene **microarray** data sets, on colon cancer and leukemia. By identifying relevant subsets of the data and focusing on them we were able to discover partitions and correlations that were masked and hidden when the full dataset was used in the analysis. Some of these partitions have clear biological interpretation; others can serve to identify possible directions for future research.

L12 ANSWER 7 OF 12 MEDLINE
ACCESSION NUMBER: 2000283715 MEDLINE
DOCUMENT NUMBER: 20283715 PubMed ID: 10821957
TITLE: **Gene expression** profiling in human peripheral blood mononuclear cells using high-density filter-based cDNA microarrays.
AUTHOR: Walker J; Rigley K
CORPORATE SOURCE: The Edward Jenner Institute for Vaccine Research, Dendritic Cell Group, Compton, RG20 7NN, Newbury, UK.
SOURCE: JOURNAL OF IMMUNOLOGICAL METHODS, (2000 May 26) 239 (1-2) 167-79.
Journal code: IFE; 1305440. ISSN: 0022-1759.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000810
Last Updated on STN: 20000810
Entered Medline: 20000721

AB **Microarray** technology has provided the ability to analyse the expression profiles for thousands of genes in parallel. The need for highly specialised equipment to use certain types of microarrays has restricted the application of this technology to a small number of dedicated laboratories. High-density filter-based cDNA microarrays provide a low-cost option for performing high-throughput **gene expression** analysis. We have used a model system in which filter-based cDNA microarrays representing over 4000 known human genes were used to monitor the kinetics of **gene expression** in human peripheral blood mononuclear cells (PBMCs) stimulated with phytohaemagluttinin (PHA). Using software-based **cluster analysis**, we identified 104 genes that altered in expression levels in response to PHA stimulation of PBMCs and showed that there was a considerable overlap between genes with similar temporal expression profiles and similar functional roles. Comparison of **microarray** quantitation with quantitative PCR showed almost identical expression profiles for a number of genes. Coupled with the fact that our findings are in agreement with a large number of independent observations, we conclude that the use of filter-based cDNA microarrays is a valid and accurate method for high-throughput **gene expression** profiling.

L12 ANSWER 8 OF 12 MEDLINE
ACCESSION NUMBER: 2000282814 MEDLINE
DOCUMENT NUMBER: 20282814 PubMed ID: 10820484
TITLE: Development of a prostate cDNA **microarray** and statistical **gene expression** analysis package.
AUTHOR: Carlisle A J; Prabhu V V; Elkahloun A; Hudson J; Trent J M; Linehan W M; Williams E D; Emmert-Buck M R; Liotta L A; Munson P J; Krizman D B
CORPORATE SOURCE: Laboratory of Pathology, National Cancer Institute, Rockville, Maryland, USA.
SOURCE: MOLECULAR CARCINOGENESIS, (2000 May) 28 (1) 12-22. Journal code: AEQ; 8811105. ISSN: 0899-1987.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000616
Last Updated on STN: 20000616
Entered Medline: 20000606

AB A cDNA **microarray** comprising 5184 different cDNAs spotted onto nylon membrane filters was developed for prostate **gene expression** studies. The clones used for arraying were identified by **cluster analysis** of > 35 000 prostate cDNA library-derived expressed sequence tags (ESTs) present in the dbEST database maintained by the National Center for Biotechnology Information. Total RNA from two cell lines, prostate line 8.4 and melanoma line UACC903, was used to make radiolabeled probe for filter hybridizations. The absolute intensity of each individual cDNA spot was determined by phosphorimager scanning and evaluated by a bioinformatics package developed specifically for analysis of cDNA **microarray** experimentation. Results indicated 89% of the genes showed intensity levels above background in prostate cells compared with only 28% in melanoma cells. Replicate probe preparations yielded results with correlation values ranging from r = 0.90 to 0.93 and coefficient of

variation ranging from 16 to 28%. Findings indicate that among others, the keratin 5 and vimentin genes were differentially expressed between these two divergent cell lines. Follow-up northern blot analysis verified these two expression changes, thereby demonstrating the reliability of this system. We report the development of a cDNA **microarray** system that is sensitive and reliable, demonstrates a low degree of variability, and is capable of determining verifiable **gene expression** differences between two distinct human cell lines. This system will prove useful for differential **gene expression** analysis in prostate-derived cells and tissue.

L12 ANSWER 9 OF 12 MEDLINE
ACCESSION NUMBER: 2000183948 MEDLINE
DOCUMENT NUMBER: 20183948 PubMed ID: 10716996
TITLE: Gene **microarray** identification of redox and mitochondrial elements that control resistance or sensitivity to apoptosis.
AUTHOR: Voehringer D W; Hirschberg D L; Xiao J; Lu Q; Roederer M; Lock C B; Herzenberg L A; Steinman L; Herzenberg L A
CORPORATE SOURCE: Department of Genetics, Stanford University School of Medicine, Stanford, CA 94305, USA.. Voehringer@stanford.edu
CONTRACT NUMBER: AI-0729015 (NIAID)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2000 Mar 14) 97 (6) 2680-5. Journal code: PV3; 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000505
Last Updated on STN: 20000505
Entered Medline: 20000425

AB Multigenic programs controlling susceptibility to apoptosis in response to ionizing radiation have not yet been defined. Here, using DNA microarrays, we show **gene expression** patterns in an apoptosis-sensitive and apoptosis-resistant murine B cell lymphoma model system both before and after irradiation. From the 11,000 genes interrogated by the arrays, two major patterns emerged. First, before radiation exposure the radioresistant LYar cells expressed significantly greater levels of message for several genes involved in regulating intracellular redox potential. Compared with LYas cells, LYar cells express 20- to 50-fold more mRNA for the tetraspanin CD53 and for fructose-1,6-bisphosphatase. Expression of both of these genes can lead to the increase of total cellular glutathione, which is the principle intracellular antioxidant and has been shown to inhibit many forms of apoptosis. A second pattern emerged after radiation, when the apoptosis-sensitive LYas cells induced rapid expression of a unique cluster of genes characterized by their involvement in mitochondrial electron transport. Some of these genes have been previously recognized as proapoptotic; however others, such as uncoupling protein 2, were not previously known to be apoptotic regulatory proteins. From these observations we propose that a multigenic program for sensitivity to apoptosis involves induction of transcripts for genes participating in mitochondrial uncoupling and loss of membrane potential. This program triggers mitochondrial release of apoptogenic factors and induces the "caspase cascade." Conversely, cells resistant to apoptosis down-regulate these biochemical pathways, while activating pathways for establishment and maintenance of high intracellular redox potential by means of elevated glutathione.

L12 ANSWER 10 OF 12 MEDLINE
ACCESSION NUMBER: 2000179478 MEDLINE
DOCUMENT NUMBER: 20179478 PubMed ID: 10712947

TITLE: Analysis of large-scale **gene expression** data.
AUTHOR: Sherlock G
CORPORATE SOURCE: Department of Genetics, Stanford University Medical Center, Stanford, 94306-5120, USA.. sherlock@genome.stanford.edu
SOURCE: CURRENT OPINION IN IMMUNOLOGY, (2000 Apr) 12 (2) 201-5.
Ref: 26
Journal code: AH1; 8900118. ISSN: 0952-7915.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000606
Last Updated on STN: 20000606
Entered Medline: 20000519

AB The advent of cDNA and oligonucleotide **microarray** technologies has led to a paradigm shift in biological investigation, such that the bottleneck in research is shifting from data generation to data analysis. Hierarchical clustering, divisive clustering, self-organizing maps and k-means clustering have all been recently used to make sense of this mass of data.

L12 ANSWER 11 OF 12 MEDLINE
ACCESSION NUMBER: 2000164307 MEDLINE
DOCUMENT NUMBER: 20164307 PubMed ID: 10700163
TITLE: Making the most of **microarray** data.
AUTHOR: Gaasterland T; Bekiranov S
SOURCE: NATURE GENETICS, (2000 Mar) 24 (3) 204-6.
Journal code: BRO; 9216904. ISSN: 1061-4036.
PUB. COUNTRY: United States
News Announcement
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000413
Last Updated on STN: 20000413
Entered Medline: 20000407

L12 ANSWER 12 OF 12 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:311998 BIOSIS
DOCUMENT NUMBER: PREV200100311998
TITLE: Characterizing the transcriptional phenotype of myeloma cells.
AUTHOR(S): Claudio, Jaime O. (1); Tang, HongChang (1); Khan, Esther Masih (1); Voralia, Michael (1); Li, Zhi Hua (1); Cukerman, Eva (1); Francisco-Pabalan, Ofelia (1); Liew, Choong-Chin (1); Stewart, A. Keith (1)
CORPORATE SOURCE: (1) Oncology, University Health Network, Toronto, ON Canada
SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 1, pp. 578a. print.
Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Although the initiating molecular event in multiple myeloma has been defined by identification of several nonrandom chromosomal translocations, the transcriptional phenotype of myeloma cells subsequent to transformation has not been fully characterized. We have therefore

analyzed the global **gene expression** of CD138+ myeloma cells from pooled patient samples. Using cDNA library construction which avoids PCR, and focuses on 5' sequence together with bioinformatic tools we have generated over 6,500 cDNA sequences. More than 13% of these genes lack a sequence match in existing databases suggesting that these represent potentially novel genes. An additional 9.5% of cDNAs matched only expressed sequence tags and 4.5% matched the sequence only of a clone from the high throughput genomic sequence database. The remaining genes include known nuclear genes representing more than 57% of all sequences analyzed. In total our Myeloma Gene Database consists of -3,600 non-redundant genes. We have classified these expressed genes according to putative functions, functional domains, and novel molecules. Among the novel genes identified are a SH3-SAM domain containing adaptor strongly expressed in hematopoietic tissues, a mitogen activated protein tyrosine phosphatase, Rho/Rac GEF homologous gene, a Twist related gene, a ser/thr kinase, a kinase of the PFTAIRE family and several zinc finger domain containing genes. Using these expressed genes, we initially constructed a prototype glass slide **microarray** consisting of 1,700 cDNAs. Hybridization of bone marrow samples from patients and a normal adult donor reference control on our myeloma **array** followed by **cluster analysis** revealed genes that have similar pattern of expression in all patients bone marrow samples. Those genes that clustered together include DEAD box protein p68 helicase, translationally controlled tumor protein, and a gene similar to Drosophila CG3328 gene product. At least two of the clustered genes were also identified at very high frequency in non biased sequence analysis. The significance of this pattern of expression in myeloma is as yet unknown, however the correlation of high throughput sequencing with **array** expression data supports the validity of **microarray** generated bioinformation and has encouraged our ongoing development of a myeloma **array** utilizing all 3,600 non redundant myeloma cDNAs characterized to date. Such an **array** may provide the basis for more clearly delineating the molecular phenotype of multiple myeloma.

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 NEWS  1           Web Page URLs for STN Seminar Schedule - N. America
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 NEWS  3  Jan 29   FSTA has been reloaded and moves to weekly updates
 NEWS  4  Feb 01   DKILIT now produced by FIZ Karlsruhe and has a new update
                   frequency
 NEWS  5  Feb 19   Access via Tymnet and SprintNet Eliminated Effective 3/31/02
 NEWS  6  Mar 08   Gene Names now available in BIOSIS
 NEWS  7  Mar 22   TOXLIT no longer available
 NEWS  8  Mar 22   TRCTHERMO no longer available
 NEWS  9  Mar 28   US Provisional Priorities searched with P in CA/CAplus
                   and USPATFULL
 NEWS 10  Mar 28   LIPINSKI/CALC added for property searching in REGISTRY
 NEWS 11  Apr 02   PAPERCHEM no longer available on STN.  Use PAPERCHEM2 instead.
 NEWS 12  Apr 08   "Ask CAS" for self-help around the clock
 NEWS 13  Apr 09   BEILSTEIN: Reload and Implementation of a New Subject Area
 NEWS 14  Apr 09   ZDB will be removed from STN
 NEWS 15  Apr 19   US Patent Applications available in IFICDB, IFIPAT, and IFIUDB
 NEWS 16  Apr 22   Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
 NEWS 17  Apr 22   BIOSIS Gene Names now available in TOXCENTER
 NEWS 18  Apr 22   Federal Research in Progress (FEDRIP) now available

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               CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP),
               AND CURRENT DISCOVER FILE IS DATED 05 FEBRUARY 2002
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 NEWS PHONE    Direct Dial and Telecommunication Network Access to STN
 NEWS WWW      CAS World Wide Web Site (general information)

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=> file .biotech
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
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FULL ESTIMATED COST                                    0.21        0.21

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=> s gene expression
   4 FILES SEARCHED...
L1      700092 GENE EXPRESSION

=> s cluster analysis
L2       21071 CLUSTER ANALYSIS

=> s l1 and l2
L3         577 L1 AND L2

=> array
ARRAY IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s array
L4      129141 ARRAY

=> s l3 and l4
L5         183 L3 AND L4

=> s microarray
L6       12481 MICROARRAY

=> s l5 and l6
L7          95 L5 AND L6

=> sl7 not p7>1999
SL7 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s l7 not py>1999
L8           0 L7 NOT PY>1999

=> s l7 not py>1998
L9           0 L7 NOT PY>1998

=> dup rem l7
PROCESSING COMPLETED FOR L7
L10          80 DUP REM L7 (15 DUPLICATES REMOVED)

=> d ti l10 1-30
```

L10 ANSWER 1 OF 80 MEDLINE
TI Differential gene regulation by the two progesterone receptor isoforms in human breast cancer cells.

L10 ANSWER 2 OF 80 MEDLINE
TI DNA **microarray** analysis of differential **gene expression** in Borrelia burgdorferi, the Lyme disease spirochete.

L10 ANSWER 3 OF 80 MEDLINE
TI Identifying pre-post chemotherapy differences in **gene expression** in breast tumours: a statistical method appropriate for this aim.

L10 ANSWER 4 OF 80 MEDLINE DUPLICATE 1
TI High-density **microarray** analysis of hippocampal **gene expression** following experimental brain injury.

L10 ANSWER 5 OF 80 MEDLINE
TI **Gene expression** profiling predicts clinical outcome of breast cancer.

L10 ANSWER 6 OF 80 MEDLINE
TI Genome-wide cDNA **microarray** screening to correlate **gene expression** profiles with sensitivity of 85 human cancer xenografts to anticancer drugs.

L10 ANSWER 7 OF 80 MEDLINE
TI Global **gene expression** profiling in Barrett's esophagus and esophageal cancer: a comparative analysis using cDNA microarrays.

L10 ANSWER 8 OF 80 MEDLINE DUPLICATE 2
TI **Microarray** detection of **gene expression** changes induced by 1,25(OH)(2)D(3) and a Ca(2+) influx-activating analog in osteoblastic ROS 17/2.8 cells.

L10 ANSWER 9 OF 80 MEDLINE DUPLICATE 3
TI Expression of cytokine- and chemokine-related genes in peripheral blood mononuclear cells from lupus patients by cDNA **array**.

L10 ANSWER 10 OF 80 MEDLINE
TI Global **gene expression** analysis of gastric cancer by oligonucleotide microarrays.

L10 ANSWER 11 OF 80 MEDLINE
TI The advantages of cDNA **microarray** as an effective tool for identification of reproductive organ-specific genes in a model legume, Lotus japonicus.

L10 ANSWER 12 OF 80 MEDLINE
TI Screening of **gene expression** profiles in gastric epithelial cells induced by Helicobacter pylori using **microarray** analysis.

L10 ANSWER 13 OF 80 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Identification of genes differentially expressed in cultured human osteoblasts versus human fibroblasts by DNA **microarray** analysis.

L10 ANSWER 14 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Methods for gene profiling arrays involving RNA or cDNA amplification

L10 ANSWER 15 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Method for selecting differentially expressed genes for use in informative nucleic acid arrays

L10 ANSWER 16 OF 80 CAPLUS COPYRIGHT 2002 ACS
TI Methods for **gene expression** profiling to diagnose disease, monitor drug therapy, identify physiological states, and identify differentially expressed genes in secretory versus proliferative endometrium

L10 ANSWER 17 OF 80 MEDLINE DUPLICATE 4
TI Bootstrapping **cluster analysis**: assessing the reliability of conclusions from **microarray** experiments.

L10 ANSWER 18 OF 80 MEDLINE
TI The consequences of chromosomal aneuploidy on **gene expression** profiles in a cell line model for prostate carcinogenesis.

L10 ANSWER 19 OF 80 MEDLINE
TI Estrogen receptor status in breast cancer is associated with remarkably distinct **gene expression** patterns.

L10 ANSWER 20 OF 80 MEDLINE DUPLICATE 5
TI Molecular profiling of transformed and metastatic murine squamous carcinoma cells by differential display and cDNA **microarray** reveals altered expression of multiple genes related to growth, apoptosis, angiogenesis, and the NF-kappaB signal pathway.

L10 ANSWER 21 OF 80 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 6
TI Papillomavirus type 16 oncogenes downregulate expression of interferon-responsive genes and upregulate proliferation-associated and NF-.kappa.B-responsive genes in cervical keratinocytes

L10 ANSWER 22 OF 80 MEDLINE
TI DNA **microarray** analysis of genes involved in p53 mediated apoptosis: activation of Apaf-1.

L10 ANSWER 23 OF 80 MEDLINE
TI New molecular phenotypes in the dst mutants of Arabidopsis revealed by DNA **microarray** analysis.

L10 ANSWER 24 OF 80 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI High-sensitivity **array** analysis of **gene expression** for the early detection of disseminated breast tumor cells in peripheral blood.

L10 ANSWER 25 OF 80 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Identification of **gene expression** patterns in superficial and invasive human bladder cancer.

L10 ANSWER 26 OF 80 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI **Gene expression** in 1-trial learning of a conditioned taste aversion.

L10 ANSWER 27 OF 80 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Distinct **gene expression** profiling in chronic lymphocytic leukemia with 11q23 deletion.

L10 ANSWER 28 OF 80 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
TI **Gene expression** profiling of B cell chronic lymphocytic leukemia reveals a homogenous phenotype related to memory B cells;
cluster analysis, DNA chip, and DNA **microarray**

L10 ANSWER 29 OF 80 CAPLUS COPYRIGHT 2002 ACS

TI Establishment of normal, terminally differentiating mouse erythroid progenitors: molecular characterization by cDNA arrays

L10 ANSWER 30 OF 80 MEDLINE
TI RNA expression in the early characterization of hepatotoxicants in Wistar rats by high-density DNA microarrays.

=> d ibib abs l10 1-10

L10 ANSWER 1 OF 80 MEDLINE
ACCESSION NUMBER: 2002106152 MEDLINE
DOCUMENT NUMBER: 21826375 PubMed ID: 11717311
TITLE: Differential gene regulation by the two progesterone receptor isoforms in human breast cancer cells.
AUTHOR: Richer Jennifer K; Jacobsen Britta M; Manning Nicole G; Abel M Greg; Wolf Douglas M; Horwitz Kathryn B
CORPORATE SOURCE: Department of Medicine/Endocrinology, University of Colorado School of Medicine, Denver, Colorado 80262, USA.. jennifer.richer@uchsc.edu
CONTRACT NUMBER: CA26869 (NCI)
DK48238 (NIDDK)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2002 Feb 15) 277 (7) 5209-18.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200203
ENTRY DATE: Entered STN: 20020212
Last Updated on STN: 20020322
Entered Medline: 20020321

AB The PR-A and PR-B isoforms of progesterone receptors (PR) have different physiological functions, and their ratio varies widely in breast cancers. To determine whether the two PR regulate different genes, we used human breast cancer cell lines engineered to express one or the other isoform. Cells were treated with progesterone in triplicate, time-separated experiments, allowing statistical analyses of **microarray gene expression** data. Of 94 progesterone-regulated genes, 65 are uniquely regulated by PR-B, 4 uniquely by PR-A, and only 25 by both. Almost half the genes encode proteins that are membrane-bound or involved in membrane-initiated signaling. We also find an important set of progesterone-regulated genes involved in mammary gland development and/or implicated in breast cancer. This first, large scale study of PR gene regulation has important implications for the measurement of PR in breast cancers and for the many clinical uses of synthetic progestins. It suggests that it is important to distinguish between the two isoforms in breast cancers and that isoform-specific genes can be used to screen for ligands that selectively modulate the activity of PR-A or PR-B. Additionally, use of natural target genes, rather than "consensus" response elements, for transcription studies should improve our understanding of steroid hormone action.

L10 ANSWER 2 OF 80 MEDLINE
ACCESSION NUMBER: 2002111052 MEDLINE
DOCUMENT NUMBER: 21819468 PubMed ID: 11830671
TITLE: DNA **microarray** analysis of differential **gene expression** in Borrelia burgdorferi, the Lyme disease spirochete.
AUTHOR: Revel Andrew T; Talaat Adel M; Norgard Michael V
CORPORATE SOURCE: Department of Microbiology, University of Texas Southwestern Medical Center, Dallas, TX 75390, USA.
CONTRACT NUMBER: AI-45538 (NIAID)

SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2002 Feb 5) 99 (3) 1562-7. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200203
ENTRY DATE: Entered STN: 20020215
Last Updated on STN: 20020308
Entered Medline: 20020307

AB DNA microarrays were used to survey the adaptive genetic responses of Borrelia burgdorferi (Bb) B31, the Lyme disease spirochete, when grown under conditions analogous to those found in unfed ticks (UTs), fed ticks (FTs), or during mammalian host adaptation (Bb in dialysis membrane chambers implanted in rats). Microarrays contained 95.4% of the predicted B31 genes, 150 (8.6%) of which were differentially regulated (changes of > or = 1.8-fold) among the three growth conditions. A substantial proportion (46%) of the differentially regulated genes encoded proteins with predicted export signals (29% from predicted lipoproteins), emphasizing the importance to Bb of modulating its extracellular proteome. For B31 cultivated at the more restrictive UT condition, **microarray** data provided evidence of a bacterial stringent response and factors that restrict cell division. A large proportion of genes were responsive to the FT growth condition, wherein increased temperature and reduced pH were prominent environmental parameters. A surprising theme, supported by **cluster analysis**, was that many of the **gene expression** changes induced during the FT growth condition were transient and largely tempered as B31 adapted to the mammalian host, suggesting that once Bb gains entry and adapts to mammalian tissues, fewer differentially regulated genes are exploited. It therefore would seem that although widely dissimilar, the UT and dialysis membrane chamber growth conditions promote more static patterns of **gene expression** in Bb. The **microarray** data thus provide a basis for formulating new testable hypotheses regarding the life cycle of Bb and attaining a more complete understanding of many aspects of Bb's complex parasitic strategies.

L10 ANSWER 3 OF 80 MEDLINE
ACCESSION NUMBER: 2002216642 MEDLINE
DOCUMENT NUMBER: 21949770 PubMed ID: 11953855
TITLE: Identifying pre-post chemotherapy differences in **gene expression** in breast tumours: a statistical method appropriate for this aim.
AUTHOR: Korn E L; McShane L M; Troendle J F; Rosenwald A; Simon R
CORPORATE SOURCE: Biometric Research Branch, EPN-8128, National Cancer Institute, National Institutes of Health, Bethesda MD 20892, USA.. korne@ctep.nci.nih.gov
SOURCE: BRITISH JOURNAL OF CANCER, (2002 Apr 8) 86 (7) 1093-6. Journal code: 0370635. ISSN: 0007-0920.
PUB. COUNTRY: Scotland: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020416
Last Updated on STN: 20020501
Entered Medline: 20020430

AB Although widely used for the analysis of **gene expression** **microarray** data, **cluster analysis** may not be the most appropriate statistical technique for some study aims. We demonstrate this by considering a previous analysis of **microarray** data obtained on breast tumour specimens, many of which were paired specimens from the same patient before and after chemotherapy. Reanalysing

the data using statistical methods that appropriately utilise the paired differences for identification of differentially expressed genes, we find 17 genes that we can confidently identify as more expressed after chemotherapy than before. These findings were not reported by the original investigators who analysed the data using **cluster analysis** techniques.

L10 ANSWER 4 OF 80 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2002159238 MEDLINE
DOCUMENT NUMBER: 21888965 PubMed ID: 11891777
TITLE: High-density **microarray** analysis of hippocampal **gene expression** following experimental brain injury.
AUTHOR: Matzilevich David A; Rall Jason M; Moore Anthony N; Grill Raymond J; Dash Pramod K
CORPORATE SOURCE: The Vivian L. Smith Center for Neurologic Research, Departments of Neurobiology and Anatomy, Neurosurgery, The University of Texas Medical School, Houston, Texas 77225, USA.
CONTRACT NUMBER: MH49662 (NIMH)
NS3545 (NINDS)
P50NS23327 (NINDS)
SOURCE: JOURNAL OF NEUROSCIENCE RESEARCH, (2002 Mar 1) 67 (5) 646-63.
Journal code: 7600111. ISSN: 0360-4012.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020314
Last Updated on STN: 20020501
Entered Medline: 20020430
AB Behavioral, biophysical, and pharmacological studies have implicated the hippocampus in the formation and storage of spatial memory. Traumatic brain injury (TBI) often causes spatial memory deficits, which are thought to arise from the death as well as the dysfunction of hippocampal neurons. Cell death and dysfunction are commonly associated with and often caused by altered expression of specific genes. The identification of the genes involved in these processes, as well as those participating in postinjury cellular repair and plasticity, is important for the development of mechanism-based therapies. To monitor the expression levels of a large number of genes and to identify genes not previously implicated in TBI pathophysiology, a high-density oligonucleotide **array** containing 8,800 genes was interrogated. RNA samples were prepared from ipsilateral hippocampi 3 hr and 24 hr following lateral cortical impact injury and compared to samples from sham-operated controls. **Cluster analysis** was employed using statistical algorithms to arrange the genes according to similarity in patterns of expression. The study indicates that the genomic response to TBI is complex, affecting approximately 6% (at the time points examined) of the total number of genes examined. The identity of the genes revealed that TBI affects many aspects of cell physiology, including oxidative stress, metabolism, inflammation, structural changes, and cellular signaling. The analysis revealed genes whose expression levels have been reported to be altered in response to injury as well as several genes not previously implicated in TBI pathophysiology.

L10 ANSWER 5 OF 80 MEDLINE
ACCESSION NUMBER: 2002099463 MEDLINE
DOCUMENT NUMBER: 21681887 PubMed ID: 11823860
TITLE: **Gene expression** profiling predicts clinical outcome of breast cancer.
COMMENT: Comment in: Nature. 2002 Jan 31;415(6871):484-5

AUTHOR: van 't Veer Laura J; Dai Hongyue; van de Vijver Marc J; He Yudong D; Hart Augustinus A M; Mao Mao; Peterse Hans L; van der Kooy Karin; Marton Matthew J; Witteveen Anke T; Schreiber George J; Kerkhoven Ron M; Roberts Chris; Linsley Peter S; Bernards Rene; Friend Stephen H
CORPORATE SOURCE: Division of Diagnostic Oncology, The Netherlands Cancer Institute, 121 Plesmanlaan, 1066 CX Amsterdam, The Netherlands.
SOURCE: NATURE, (2002 Jan 31) 415 (6871) 530-6.
Journal code: 0410462. ISSN: 0028-0836.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200203
ENTRY DATE: Entered STN: 20020207
Last Updated on STN: 20020313
Entered Medline: 20020312

AB Breast cancer patients with the same stage of disease can have markedly different treatment responses and overall outcome. The strongest predictors for metastases (for example, lymph node status and histological grade) fail to classify accurately breast tumours according to their clinical behaviour. Chemotherapy or hormonal therapy reduces the risk of distant metastases by approximately one-third; however, 70-80% of patients receiving this treatment would have survived without it. None of the signatures of breast cancer **gene expression** reported to date allow for patient-tailored therapy strategies. Here we used DNA **microarray** analysis on primary breast tumours of 117 young patients, and applied supervised classification to identify a **gene expression** signature strongly predictive of a short interval to distant metastases ('poor prognosis' signature) in patients without tumour cells in local lymph nodes at diagnosis (lymph node negative). In addition, we established a signature that identifies tumours of BRCA1 carriers. The poor prognosis signature consists of genes regulating cell cycle, invasion, metastasis and angiogenesis. This **gene expression** profile will outperform all currently used clinical parameters in predicting disease outcome. Our findings provide a strategy to select patients who would benefit from adjuvant therapy.

L10 ANSWER 6 OF 80 MEDLINE
ACCESSION NUMBER: 2002082994 MEDLINE
DOCUMENT NUMBER: 21668025 PubMed ID: 11809704
TITLE: Genome-wide cDNA **microarray** screening to correlate **gene expression** profiles with sensitivity of 85 human cancer xenografts to anticancer drugs.
AUTHOR: Zembutsu Hitoshi; Ohnishi Yasuyuki; Tsunoda Tatsuhiko; Furukawa Yoichi; Katagiri Toyomasa; Ueyama Yoshito; Tamaoki Norikazu; Nomura Tatsuji; Kitahara Osamu; Yanagawa Rempei; Hirata Koichi; Nakamura Yusuke
CORPORATE SOURCE: Laboratory of Molecular Medicine, Human Genome Center, Institute of Medical Science, The University of Tokyo, Tokyo 108-8639, Japan.
SOURCE: CANCER RESEARCH, (2002 Jan 15) 62 (2) 518-27.
Journal code: 2984705R. ISSN: 0008-5472.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20020128
Last Updated on STN: 20020216
Entered Medline: 20020215

AB One of the most critical issues to be solved in regard to cancer

chemotherapy is the need to establish a method for predicting efficacy or toxicity of anticancer drugs for individual patients. To identify genes that might be associated with chemosensitivity, we used a cDNA **microarray** representing 23,040 genes to analyze expression profiles in a panel of 85 cancer xenografts derived from nine human organs. The xenografts, implanted into nude mice, were examined for sensitivity to nine anticancer drugs (5-fluorouracil, 3-[(4-amino-2-methyl-5-pyrimidinyl)methyl]-1-(2-chloroethyl)-1-nitrosourea hydrochloride, adriamycin, cyclophosphamide, cisplatin, mitomycin C, methotrexate, vincristine, and vinblastine). Comparison of the **gene expression** profiles of the tumors with sensitivities to each drug identified 1,578 genes whose expression levels correlated significantly with chemosensitivity; 333 of those genes showed significant correlation with two or more drugs, and 32 correlated with six or seven drugs. These data should contribute useful information for identifying predictive markers for drug sensitivity that may eventually provide "personalized chemotherapy" for individual patients, as well as for development of novel drugs to overcome acquired resistance of tumor cells to chemical agents.

L10 ANSWER 7 OF 80 MEDLINE
ACCESSION NUMBER: 2002091288 MEDLINE
DOCUMENT NUMBER: 21679760 PubMed ID: 11821959
TITLE: Global **gene expression** profiling in Barrett's esophagus and esophageal cancer: a comparative analysis using cDNA microarrays.
AUTHOR: Selaru F M; Zou T; Xu Y; Shustova V; Yin J; Mori Y; Sato F; Wang S; Olaru A; Shibata D; Greenwald B D; Krasna M J; Abraham J M; Meltzer S J
CORPORATE SOURCE: Department of Medicine, Division of Gastroenterology, Greenebaum Cancer Center, University of Maryland School of Medicine, Baltimore VA Hospital, MD 21201, USA.
CONTRACT NUMBER: CA77057 (NCI)
CA85069 (NCI)
CA95323 (NCI)
DK47717 (NIDDK)
SOURCE: ONCOGENE, (2002 Jan 17) 21 (3) 475-8.
Journal code: 8711562. ISSN: 0950-9232.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20020201
Last Updated on STN: 20020215
Entered Medline: 20020214

AB In order to identify and contrast global **gene expression** profiles defining the premalignant syndrome, Barrett's esophagus, as well as frank esophageal cancer, we utilized cDNA **microarray** technology in conjunction with bioinformatics tools. We hybridized microarrays, each containing 8000 cDNA clones, to RNAs extracted from 13 esophageal surgical or endoscopic biopsy specimens (seven Barrett's metaplasias and six esophageal carcinomas). Hierarchical **cluster analysis** was performed on these results and displayed using a color-coded graphic representation (Treeview). The esophageal samples clustered naturally into two principal groups, each possessing unique global **gene expression** profiles. After retrieving histologic reports for these tissues, we found that one main cluster contained all seven Barrett's samples, while the remaining principal cluster comprised the six esophageal cancers. The cancers also clustered according to histopathological subtype. Thus, squamous cell carcinomas (SCCAs) constituted one group, adenocarcinomas (ADCAs) clustered separately, and one signet-ring carcinoma was in its own cluster, distinct from the ADCA cluster. We conclude that cDNA microarrays and bioinformatics show promise in the classification of esophageal malignant

and premalignant diseases, and that these methods can be applied to small biopsy samples.

L10 ANSWER 8 OF 80 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2002225478 IN-PROCESS
DOCUMENT NUMBER: 21959637 PubMed ID: 11960622
TITLE: **Microarray** detection of **gene expression** changes induced by 1,25(OH)(2)D(3) and a Ca(2+) influx-activating analog in osteoblastic ROS 17/2.8 cells.
AUTHOR: Farach-Carson Mary C; Xu Yihuan
CORPORATE SOURCE: Department of Biological Sciences, 51 E. Main Street, University of Delaware, 19716, Newark, DE, USA.
SOURCE: STEROIDS, (2002 May) 67 (6) 467-70.
Journal code: 0404536. ISSN: 0039-128X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020419
Last Updated on STN: 20020419
AB 1,25-Dihydroxyvitamin D(3) (1,25(OH)(2)D(3)) treatment of osteoblastic ROS 17/2.8 cells initiates membrane-initiated rapid responses through activation of Ca(2+) influx and longer-term nuclear receptor-mediated changes in **gene expression**. Ca(2+) influx triggers a change in the phosphorylation state of the bone matrix protein, osteopontin (OPN), detectable at 3 h and prior to nuclear receptor-mediated events. This study aimed to determine if Ca(2+) influx induced by 1,25(OH)(2)D(3) would produce nuclear receptor-independent changes in **gene expression**. We employed a rat cDNA **microarray** strategy to screen the transcriptional changes at 3 h of treatment with 1,25(OH)(2)D(3) and with an analog of 1,25(OH)(2)D(3) (25(OH)-16ene-23yne-D(3) [AT]) that we previously showed to activate Ca(2+) influx without binding to the nuclear receptor. Arrays also were screened with cDNA from ROS 17/2.8 cells treated for 24 h, when nuclear receptor-mediated transcriptional events would occur. Rat gene filters (GeneFilter, Research Genetics) were hybridized with labeled cDNA probes from treatment groups. Among 5000 different clones on the **array** filters, we identified a family of genes which were altered 2-fold or greater following treatment with 1,25(OH)(2)D(3) or analog AT for 3 h. **Cluster analysis** also revealed genes whose expression was significantly up-regulated at 24 h, including OPN. Analysis of rapid changes in **gene expression** revealed changes affecting a diverse range of cellular pathways and functions, including protein kinases and phosphatases, Ca(2+) signaling, cell adhesion and secretion. These findings provide clear evidence of rapid changes in **gene expression** associated with Ca(2+) influx mediated by 1,25(OH)(2)D(3), and shed light on the nuclear-receptor independent signaling pathway affecting OPN phosphorylation.

L10 ANSWER 9 OF 80 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2002159638 MEDLINE
DOCUMENT NUMBER: 21888419 PubMed ID: 11890715
TITLE: Expression of cytokine- and chemokine-related genes in peripheral blood mononuclear cells from lupus patients by cDNA **array**.
AUTHOR: Rus Violeta; Atamas Sergei P; Shustova Valentina; Luzina Irina G; Selaru Florin; Magder Laurence S; Via Charles S
CORPORATE SOURCE: Division of Rheumatology and Clinical Immunology, Department of Medicine, University of Maryland Medical School, Baltimore, Maryland 21201, USA.. vrus@umaryland.edu
CONTRACT NUMBER: 1 K23 AR02135-01A1 (NIAMS)
1R03AR47110 (NIAMS)
SOURCE: CLINICAL IMMUNOLOGY, (2002 Mar) 102 (3) 283-90.

Journal code: 100883537. ISSN: 1521-6616.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020314
Last Updated on STN: 20020418
Entered Medline: 20020417

AB Systemic lupus erythematosus (SLE) is characterized by diverse and complex immune abnormalities. In an effort to begin to characterize the full complexity of immune abnormalities, the expression pattern of 375 potentially relevant genes was analyzed using peripheral blood mononuclear cells (PBMC) from 21 SLE patients and 12 controls by cDNA arrays. When mean **gene expression** for patients was compared to controls, 50 genes were identified that exhibited more than 2.5-fold difference in expression level. By the Mann-Whitney U test, 20 genes were significantly different ($P < 0.05$) between patients and controls. Most of these genes have not been previously associated with SLE and belong to a variety of families such as TNF/death receptor, IL-1 cytokine family, and IL-8 and its receptors. Hierarchical clustering of samples and differentially expressed genes revealed that with few exceptions, patients clustered separately from controls. These results highlight the potential use of the **microarray** data in identifying genes associated with SLE, which could become candidate molecular markers or future therapeutic targets.

L10 ANSWER 10 OF 80 MEDLINE
ACCESSION NUMBER: 2002086022 MEDLINE
DOCUMENT NUMBER: 21642071 PubMed ID: 11782383
TITLE: Global **gene expression** analysis of gastric cancer by oligonucleotide microarrays.
AUTHOR: Hippo Yoshitaka; Taniguchi Hirokazu; Tsutsumi Shuichi; Machida Naoko; Chong Ja-Mun; Fukayama Masashi; Kodama Tatsuhiko; Aburatani Hiroyuki
CORPORATE SOURCE: Genome Science Division, The University of Tokyo, Tokyo 153-8904, Japan.
SOURCE: CANCER RESEARCH, (2002 Jan 1) 62 (1) 233-40.
Journal code: 2984705R. ISSN: 0008-5472.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20020130
Last Updated on STN: 20020213
Entered Medline: 20020212

AB To gain molecular understanding of carcinogenesis, progression, and diversity of gastric cancer, 22 primary human advanced gastric cancer tissues and 8 noncancerous gastric tissues were analyzed by high-density oligonucleotide **microarray** in this study. Based on expression analysis of approximately 6800 genes, a two-way clustering algorithm successfully distinguished cancer tissues from noncancerous tissues. Subsequently, genes that were differentially expressed in cancer and noncancerous tissues were identified; 162 and 129 genes were highly expressed ($P < 0.05$) >2.5-fold in cancer tissues and noncancerous tissues, respectively. In cancer tissues, genes related to cell cycle, growth factor, cell motility, cell adhesion, and matrix remodeling were highly expressed. In noncancerous tissues, genes related to gastrointestinal-specific function and immune response were highly expressed. Furthermore, we identified several genes associated with lymph node metastasis including Oct-2 or histological types including Liver-Intestine Cadherin. These results provide not only a new molecular basis for understanding biological properties of gastric cancer, but also useful resources for

future development of therapeutic targets and diagnostic markers for gastric cancer.

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(FILE 'HOME' ENTERED AT 15:41:16 ON 09 MAY 2002)

FILE 'MEDLINE, BIOSIS, BIOTECHDS, CAPLUS, EMBASE' ENTERED AT 15:41:24 ON 09 MAY 2002

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L1        700092 S GENE EXPRESSION
L2         21071 S CLUSTER ANALYSIS
L3           577 S L1 AND L2
L4        129141 S ARRAY
L5           183 S L3 AND L4
L6         12481 S MICROARRAY
L7            95 S L5 AND L6
L8             0 S L7 NOT PY>1999
L9             0 S L7 NOT PY>1998
L10           80 DUP REM L7 (15 DUPLICATES REMOVED)

=> dup rem l10
PROCESSING COMPLETED FOR L10
L11           80 DUP REM L10 (0 DUPLICATES REMOVED)

=> s l11 not py>2000
L12           12 L11 NOT PY>2000

=> d ti l12

L12  ANSWER 1 OF 12     MEDLINE
TI   Assessing reliability of gene clusters from gene
     expression data.


=> d ibib abs l12 1-12

L12  ANSWER 1 OF 12     MEDLINE
ACCESSION NUMBER:   2002065931     MEDLINE
DOCUMENT NUMBER:    21652689   PubMed ID: 11793234
TITLE:              Assessing reliability of gene clusters from gene
                    expression data.
AUTHOR:             Zhang K; Zhao H
CORPORATE SOURCE:   Department of Epidemiology and Public Health, Yale
                    University School of Medicine, New Haven, CT 06520, USA.
CONTRACT NUMBER:    HD36834 (NICHD)
                    MG59507
SOURCE:             Funct Integr Genomics, (2000 Nov) 1 (3) 156-73.
                    Journal code: 100939343. ISSN: 1438-793X.
PUB. COUNTRY:       Germany: Germany, Federal Republic of
                    Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        200203
ENTRY DATE:         Entered STN: 20020125
                    Last Updated on STN: 20020307
                    Entered Medline: 20020305
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AB The rapid development of **microarray** technologies has raised many challenging problems in experiment design and data analysis. Although many numerical algorithms have been successfully applied to analyze **gene expression** data, the effects of variations and uncertainties in measured **gene expression** levels across samples and experiments have been largely ignored in the literature. In this article, in the context of hierarchical clustering

algorithms, we introduce a statistical resampling method to assess the reliability of gene clusters identified from any hierarchical clustering method. Using the clustering trees constructed from the resampled data, we can evaluate the confidence value for each node in the observed clustering tree. A majority-rule consensus tree can be obtained, showing clusters that only occur in a majority of the resampled trees. We illustrate our proposed methods with applications to two published data sets. Although the methods are discussed in the context of hierarchical clustering methods, they can be applied with other cluster-identification methods for **gene expression** data to assess the reliability of any gene cluster of interest.

L12 ANSWER 2 OF 12 MEDLINE
ACCESSION NUMBER: 2001646598 MEDLINE
DOCUMENT NUMBER: 21557040 PubMed ID: 11700594
TITLE: Cluster inference methods and graphical models evaluated on NCI60 **microarray gene expression** data.
AUTHOR: Waddell P J; Kishino H
CORPORATE SOURCE: Chugai Research Institute for Molecular Medicine, 153-2 Nagai Niihari Ibaraki 300-4101, Japan.. waddell@cimmed.com
SOURCE: GENOME INFORMATICS SERIES, (2000) 11 129-40.
Journal code: 9717234. ISSN: 0919-9454.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011112
Last Updated on STN: 20020124
Entered Medline: 20011231

AB At present, there is a lack of a sound methodology to infer causal **gene expression** relationships on a genome wide basis. We address this first by examining the behaviour of some of the latest and fastest algorithms for tree and **cluster analysis**, particularly hierarchical methods popular in phylogenetics. Combined with these are two novel distances based on partial, rather than full, correlations. Theoretically, partial correlations should provide better evidence for regulatory genetic links than standard correlations. To compare the clusters obtained by many alternative methods we use tree consensus methods. To compare methods of analysis we used tree partition metrics followed by another level of clustering. These, and a tree fit metric, all suggest that the new distances give quite different trees than those usually obtained. In the second part we consider graphical modeling of the interactions of important genes of the cell cycle. Despite the models seeming to fit well on occasions, and despite the experimental error structure seeming close to multivariate normal, there are considerable problems to overcome. Latent variables, in this case important genes missing from the analysis, are inferred to have a strong effect on the partial correlations. Also, the data show clear evidence of sampling distributions conditional on the status of important cancer related genes, including TP53. Without full information on which genes are wild type the appropriate models cannot be fitted. These findings point to the need to include and distinguish not only all relevant genes but also all splice variants in the design phase of a **microarray** analysis. Failure to do so will induce problems similar to both latent variables and conditional distributions.

L12 ANSWER 3 OF 12 MEDLINE
ACCESSION NUMBER: 2001382141 MEDLINE
DOCUMENT NUMBER: 21148270 PubMed ID: 11250685
TITLE: **Microarray** foray.
AUTHOR: Coffey R J; Threadgill D
SOURCE: Breast Cancer Res, (2000) 2 (1) 8-9. Ref: 5

Journal code: DYZ; 100927353. ISSN: 1465-5411.
PUB. COUNTRY: England: United Kingdom
Editorial
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200107
ENTRY DATE: Entered STN: 20010709
Last Updated on STN: 20010709
Entered Medline: 20010705

L12 ANSWER 4 OF 12 MEDLINE
ACCESSION NUMBER: 2001102281 MEDLINE
DOCUMENT NUMBER: 20431605 PubMed ID: 10977093
TITLE: Genes, themes and microarrays: using information retrieval for large-scale gene analysis.
AUTHOR: Shatkay H; Edwards S; Wilbur W J; Boguski M
CORPORATE SOURCE: National Center for Biotechnology Information, NLM, NIH, Bethesda, Maryland 20984, USA.. shatkay@ncbi.nlm.nih.gov
SOURCE: ISMB, (2000) 8 317-28.
Journal code: CCP.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010126

AB The immense volume of data resulting from DNA **microarray** experiments, accompanied by an increase in the number of publications discussing gene-related discoveries, presents a major data analysis challenge. Current methods for genome-wide analysis of expression data typically rely on **cluster analysis** of **gene expression** patterns. Clustering indeed reveals potentially meaningful relationships among genes, but can not explain the underlying biological mechanisms. In an attempt to address this problem, we have developed a new approach for utilizing the literature in order to establish functional relationships among genes on a genome-wide scale. Our method is based on revealing coherent themes within the literature, using a similarity-based search in document space. Content-based relationships among abstracts are then translated into functional connections among genes. We describe preliminary experiments applying our algorithm to a database of documents discussing yeast genes. A comparison of the produced results with well-established yeast gene functions demonstrates the effectiveness of our approach.

L12 ANSWER 5 OF 12 MEDLINE
ACCESSION NUMBER: 2001071436 MEDLINE
DOCUMENT NUMBER: 20553126 PubMed ID: 11101835
TITLE: The transcriptome of Arabidopsis thaliana during systemic acquired resistance.
AUTHOR: Maleck K; Levine A; Eulgem T; Morgan A; Schmid J; Lawton K A; Dangl J L; Dietrich R A
CORPORATE SOURCE: Syngenta, Research Triangle Park, North Carolina, USA.
SOURCE: NATURE GENETICS, (2000 Dec) 26 (4) 403-10.
Journal code: BRO. ISSN: 1061-4036.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322

Last Updated on STN: 20010322
Entered Medline: 20010104

AB Infected plants undergo transcriptional reprogramming during initiation of both local defence and systemic acquired resistance (SAR). We monitored **gene-expression** changes in Arabidopsis thaliana under 14 different SAR-inducing or SAR-repressing conditions using a DNA **microarray** representing approximately 25-30% of all A. thaliana genes. We derived groups of genes with common regulation patterns, or regulons. The regulon containing PR-1, a reliable marker gene for SAR in A. thaliana, contains known PR genes and novel genes likely to function during SAR and disease resistance. We identified a common promoter element in genes of this regulon that binds members of a plant-specific transcription factor family. Our results extend expression profiling to definition of regulatory networks and gene discovery in plants.

L12 ANSWER 6 OF 12 MEDLINE
ACCESSION NUMBER: 2001039008 MEDLINE
DOCUMENT NUMBER: 20504466 PubMed ID: 11035779
TITLE: Coupled two-way clustering analysis of gene **microarray** data.
AUTHOR: Getz G; Levine E; Domany E
CORPORATE SOURCE: Department of Physics of Complex Systems, Weizmann Institute of Science, Rehovot 76100, Israel.
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2000 Oct 24) 97 (22) 12079-84.
Journal code: PV3. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200011
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001128

AB We present a coupled two-way clustering approach to gene **microarray** data analysis. The main idea is to identify subsets of the genes and samples, such that when one of these is used to cluster the other, stable and significant partitions emerge. The search for such subsets is a computationally complex task. We present an algorithm, based on iterative clustering, that performs such a search. This analysis is especially suitable for gene **microarray** data, where the contributions of a variety of biological mechanisms to the **gene expression** levels are entangled in a large body of experimental data. The method was applied to two gene **microarray** data sets, on colon cancer and leukemia. By identifying relevant subsets of the data and focusing on them we were able to discover partitions and correlations that were masked and hidden when the full dataset was used in the analysis. Some of these partitions have clear biological interpretation; others can serve to identify possible directions for future research.

L12 ANSWER 7 OF 12 MEDLINE
ACCESSION NUMBER: 2000283715 MEDLINE
DOCUMENT NUMBER: 20283715 PubMed ID: 10821957
TITLE: **Gene expression** profiling in human peripheral blood mononuclear cells using high-density filter-based cDNA microarrays.
AUTHOR: Walker J; Rigley K
CORPORATE SOURCE: The Edward Jenner Institute for Vaccine Research, Dendritic Cell Group, Compton, RG20 7NN, Newbury, UK.
SOURCE: JOURNAL OF IMMUNOLOGICAL METHODS, (2000 May 26) 239 (1-2) 167-79.
Journal code: IFE; 1305440. ISSN: 0022-1759.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000810
Last Updated on STN: 20000810
Entered Medline: 20000721

AB **Microarray** technology has provided the ability to analyse the expression profiles for thousands of genes in parallel. The need for highly specialised equipment to use certain types of microarrays has restricted the application of this technology to a small number of dedicated laboratories. High-density filter-based cDNA microarrays provide a low-cost option for performing high-throughput **gene expression** analysis. We have used a model system in which filter-based cDNA microarrays representing over 4000 known human genes were used to monitor the kinetics of **gene expression** in human peripheral blood mononuclear cells (PBMCs) stimulated with phytohaemagluttinin (PHA). Using software-based **cluster analysis**, we identified 104 genes that altered in expression levels in response to PHA stimulation of PBMCs and showed that there was a considerable overlap between genes with similar temporal expression profiles and similar functional roles. Comparison of **microarray** quantitation with quantitative PCR showed almost identical expression profiles for a number of genes. Coupled with the fact that our findings are in agreement with a large number of independent observations, we conclude that the use of filter-based cDNA microarrays is a valid and accurate method for high-throughput **gene expression** profiling.

L12 ANSWER 8 OF 12 MEDLINE
ACCESSION NUMBER: 2000282814 MEDLINE
DOCUMENT NUMBER: 20282814 PubMed ID: 10820484
TITLE: Development of a prostate cDNA **microarray** and statistical **gene expression** analysis package.
AUTHOR: Carlisle A J; Prabhu V V; Elkahloun A; Hudson J; Trent J M; Linehan W M; Williams E D; Emmert-Buck M R; Liotta L A; Munson P J; Krizman D B
CORPORATE SOURCE: Laboratory of Pathology, National Cancer Institute, Rockville, Maryland, USA.
SOURCE: MOLECULAR CARCINOGENESIS, (2000 May) 28 (1) 12-22. Journal code: AEQ; 8811105. ISSN: 0899-1987.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000616
Last Updated on STN: 20000616
Entered Medline: 20000606

AB A cDNA **microarray** comprising 5184 different cDNAs spotted onto nylon membrane filters was developed for prostate **gene expression** studies. The clones used for arraying were identified by **cluster analysis** of > 35 000 prostate cDNA library-derived expressed sequence tags (ESTs) present in the dbEST database maintained by the National Center for Biotechnology Information. Total RNA from two cell lines, prostate line 8.4 and melanoma line UACC903, was used to make radiolabeled probe for filter hybridizations. The absolute intensity of each individual cDNA spot was determined by phosphorimager scanning and evaluated by a bioinformatics package developed specifically for analysis of cDNA **microarray** experimentation. Results indicated 89% of the genes showed intensity levels above background in prostate cells compared with only 28% in melanoma cells. Replicate probe preparations yielded results with correlation values ranging from r = 0.90 to 0.93 and coefficient of

variation ranging from 16 to 28%. Findings indicate that among others, the keratin 5 and vimentin genes were differentially expressed between these two divergent cell lines. Follow-up northern blot analysis verified these two expression changes, thereby demonstrating the reliability of this system. We report the development of a cDNA **microarray** system that is sensitive and reliable, demonstrates a low degree of variability, and is capable of determining verifiable **gene expression** differences between two distinct human cell lines. This system will prove useful for differential **gene expression** analysis in prostate-derived cells and tissue.

L12 ANSWER 9 OF 12 MEDLINE
ACCESSION NUMBER: 2000183948 MEDLINE
DOCUMENT NUMBER: 20183948 PubMed ID: 10716996
TITLE: Gene **microarray** identification of redox and mitochondrial elements that control resistance or sensitivity to apoptosis.
AUTHOR: Voehringer D W; Hirschberg D L; Xiao J; Lu Q; Roederer M; Lock C B; Herzenberg L A; Steinman L; Herzenberg L A
CORPORATE SOURCE: Department of Genetics, Stanford University School of Medicine, Stanford, CA 94305, USA.. Voehringer@stanford.edu
CONTRACT NUMBER: AI-0729015 (NIAID)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2000 Mar 14) 97 (6) 2680-5. Journal code: PV3; 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000505
Last Updated on STN: 20000505
Entered Medline: 20000425

AB Multigenic programs controlling susceptibility to apoptosis in response to ionizing radiation have not yet been defined. Here, using DNA microarrays, we show **gene expression** patterns in an apoptosis-sensitive and apoptosis-resistant murine B cell lymphoma model system both before and after irradiation. From the 11,000 genes interrogated by the arrays, two major patterns emerged. First, before radiation exposure the radioresistant LYar cells expressed significantly greater levels of message for several genes involved in regulating intracellular redox potential. Compared with LYas cells, LYar cells express 20- to 50-fold more mRNA for the tetraspanin CD53 and for fructose-1,6-bisphosphatase. Expression of both of these genes can lead to the increase of total cellular glutathione, which is the principle intracellular antioxidant and has been shown to inhibit many forms of apoptosis. A second pattern emerged after radiation, when the apoptosis-sensitive LYas cells induced rapid expression of a unique cluster of genes characterized by their involvement in mitochondrial electron transport. Some of these genes have been previously recognized as proapoptotic; however others, such as uncoupling protein 2, were not previously known to be apoptotic regulatory proteins. From these observations we propose that a multigenic program for sensitivity to apoptosis involves induction of transcripts for genes participating in mitochondrial uncoupling and loss of membrane potential. This program triggers mitochondrial release of apoptogenic factors and induces the "caspase cascade." Conversely, cells resistant to apoptosis down-regulate these biochemical pathways, while activating pathways for establishment and maintenance of high intracellular redox potential by means of elevated glutathione.

L12 ANSWER 10 OF 12 MEDLINE
ACCESSION NUMBER: 2000179478 MEDLINE
DOCUMENT NUMBER: 20179478 PubMed ID: 10712947

TITLE: Analysis of large-scale **gene expression** data.
AUTHOR: Sherlock G
CORPORATE SOURCE: Department of Genetics, Stanford University Medical Center, Stanford, 94306-5120, USA.. sherlock@genome.stanford.edu
SOURCE: CURRENT OPINION IN IMMUNOLOGY, (2000 Apr) 12 (2) 201-5.
Ref: 26
Journal code: AH1; 8900118. ISSN: 0952-7915.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000606
Last Updated on STN: 20000606
Entered Medline: 20000519

AB The advent of cDNA and oligonucleotide **microarray** technologies has led to a paradigm shift in biological investigation, such that the bottleneck in research is shifting from data generation to data analysis. Hierarchical clustering, divisive clustering, self-organizing maps and k-means clustering have all been recently used to make sense of this mass of data.

L12 ANSWER 11 OF 12 MEDLINE
ACCESSION NUMBER: 2000164307 MEDLINE
DOCUMENT NUMBER: 20164307 PubMed ID: 10700163
TITLE: Making the most of **microarray** data.
AUTHOR: Gaasterland T; Bekiranov S
SOURCE: NATURE GENETICS, (2000 Mar) 24 (3) 204-6.
Journal code: BRO; 9216904. ISSN: 1061-4036.
PUB. COUNTRY: United States
News Announcement
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000413
Last Updated on STN: 20000413
Entered Medline: 20000407

L12 ANSWER 12 OF 12 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:311998 BIOSIS
DOCUMENT NUMBER: PREV200100311998
TITLE: Characterizing the transcriptional phenotype of myeloma cells.
AUTHOR(S): Claudio, Jaime O. (1); Tang, HongChang (1); Khan, Esther Masih (1); Voralia, Michael (1); Li, Zhi Hua (1); Cukerman, Eva (1); Francisco-Pabalan, Ofelia (1); Liew, Choong-Chin (1); Stewart, A. Keith (1)
CORPORATE SOURCE: (1) Oncology, University Health Network, Toronto, ON Canada
SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 1, pp. 578a. print.
Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Although the initiating molecular event in multiple myeloma has been defined by identification of several nonrandom chromosomal translocations, the transcriptional phenotype of myeloma cells subsequent to transformation has not been fully characterized. We have therefore

analyzed the global **gene expression** of CD138+ myeloma cells from pooled patient samples. Using cDNA library construction which avoids PCR, and focuses on 5' sequence together with bioinformatic tools we have generated over 6,500 cDNA sequences. More than 13% of these genes lack a sequence match in existing databases suggesting that these represent potentially novel genes. An additional 9.5% of cDNAs matched only expressed sequence tags and 4.5% matched the sequence only of a clone from the high throughput genomic sequence database. The remaining genes include known nuclear genes representing more than 57% of all sequences analyzed. In total our Myeloma Gene Database consists of -3,600 non-redundant genes. We have classified these expressed genes according to putative functions, functional domains, and novel molecules. Among the novel genes identified are a SH3-SAM domain containing adaptor strongly expressed in hematopoietic tissues, a mitogen activated protein tyrosine phosphatase, Rho/Rac GEF homologous gene, a Twist related gene, a ser/thr kinase, a kinase of the PFTAIRE family and several zinc finger domain containing genes. Using these expressed genes, we initially constructed a prototype glass slide **microarray** consisting of 1,700 cDNAs. Hybridization of bone marrow samples from patients and a normal adult donor reference control on our myeloma **array** followed by **cluster analysis** revealed genes that have similar pattern of expression in all patients bone marrow samples. Those genes that clustered together include DEAD box protein p68 helicase, translationally controlled tumor protein, and a gene similar to Drosophila CG3328 gene product. At least two of the clustered genes were also identified at very high frequency in non biased sequence analysis. The significance of this pattern of expression in myeloma is as yet unknown, however the correlation of high throughput sequencing with **array** expression data supports the validity of **microarray** generated bioinformation and has encouraged our ongoing development of a myeloma **array** utilizing all 3,600 non redundant myeloma cDNAs characterized to date. Such an **array** may provide the basis for more clearly delineating the molecular phenotype of multiple myeloma.

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=> d his

     (FILE 'HOME' ENTERED AT 15:41:16 ON 09 MAY 2002)

     FILE 'MEDLINE, BIOSIS, BIOTECHDS, CAPLUS, EMBASE' ENTERED AT 15:41:24 ON
     09 MAY 2002
L1       700092 S GENE EXPRESSION
L2        21071 S CLUSTER ANALYSIS
L3          577 S L1 AND L2
L4       129141 S ARRAY
L5          183 S L3 AND L4
L6        12481 S MICROARRAY
L7           95 S L5 AND L6
L8            0 S L7 NOT PY>1999
L9            0 S L7 NOT PY>1998
L10          80 DUP REM L7 (15 DUPLICATES REMOVED)
L11          80 DUP REM L10 (0 DUPLICATES REMOVED)
L12          12 S L11 NOT PY>2000

=> s l11 not py>1999
L13           0 L11 NOT PY>1999

=> s l11 not py>2002
L14          80 L11 NOT PY>2002

=> s l11 not py>2001
L15          67 L11 NOT PY>2001

=> s l11 not py>1998
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L16           0 L11 NOT PY>1998

=> d his

     (FILE 'HOME' ENTERED AT 15:41:16 ON 09 MAY 2002)

     FILE 'MEDLINE, BIOSIS, BIOTECHDS, CAPLUS, EMBASE' ENTERED AT 15:41:24 ON
     09 MAY 2002
L1        700092 S GENE EXPRESSION
L2         21071 S CLUSTER ANALYSIS
L3           577 S L1 AND L2
L4        129141 S ARRAY
L5           183 S L3 AND L4
L6         12481 S MICROARRAY
L7            95 S L5 AND L6
L8             0 S L7 NOT PY>1999
L9             0 S L7 NOT PY>1998
L10           80 DUP REM L7 (15 DUPLICATES REMOVED)
L11           80 DUP REM L10 (0 DUPLICATES REMOVED)
L12           12 S L11 NOT PY>2000
L13            0 S L11 NOT PY>1999
L14           80 S L11 NOT PY>2002
L15           67 S L11 NOT PY>2001
L16            0 S L11 NOT PY>1998

=> s l2 and l6
L17          276 L2 AND L6

=> s l17 not py>1999
L18           8 L17 NOT PY>1999

=> d ibib abs l18 1-8

L18  ANSWER 1 OF 8     MEDLINE
ACCESSION NUMBER:    1999297564     MEDLINE
DOCUMENT NUMBER:     99297564   PubMed ID: 10371154
TITLE:               Analysis of gene expression data using self-organizing
                     maps.
AUTHOR:              Toronen P; Kolehmainen M; Wong G; Castren E
CORPORATE SOURCE:    A.I. Virtanen Institute, University of Kuopio, Finland.
SOURCE:              FEBS LETTERS, (1999 May 21) 451 (2) 142-6.
                     Journal code: EUH; 0155157. ISSN: 0014-5793.
PUB. COUNTRY:        Netherlands
                     Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
ENTRY MONTH:         199907
ENTRY DATE:          Entered STN: 19990715
                     Last Updated on STN: 19990715
                     Entered Medline: 19990706
AB   DNA microarray technologies together with rapidly increasing
     genomic sequence information is leading to an explosion in available gene
     expression data. Currently there is a great need for efficient methods to
     analyze and visualize these massive data sets. A self-organizing map (SOM)
     is an unsupervised neural network learning algorithm which has been
     successfully used for the analysis and organization of large data files.
     We have here applied the SOM algorithm to analyze published data of yeast
     gene expression and show that SOM is an excellent tool for the analysis
     and visualization of gene expression profiles.

L18  ANSWER 2 OF 8     MEDLINE
ACCESSION NUMBER:    1999061959     MEDLINE
DOCUMENT NUMBER:     99061959   PubMed ID: 9843981
TITLE:               Cluster analysis and display of
```

genome-wide expression patterns.
AUTHOR: Eisen M B; Spellman P T; Brown P O; Botstein D
CORPORATE SOURCE: Department of Genetics, Stanford University School of Medicine, 300 Pasteur Avenue, Stanford, CA 94305, USA.
CONTRACT NUMBER: CA46406 (NCI)
CA77097 (NCI)
HG00983 (NHGRI)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1998 Dec 8) 95 (25) 14863-8. Journal code: PV3; 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199901
ENTRY DATE: Entered STN: 19990128
Last Updated on STN: 20000303
Entered Medline: 19990114

AB A system of **cluster analysis** for genome-wide expression data from DNA **microarray** hybridization is described that uses standard statistical algorithms to arrange genes according to similarity in pattern of gene expression. The output is displayed graphically, conveying the clustering and the underlying expression data simultaneously in a form intuitive for biologists. We have found in the budding yeast Saccharomyces cerevisiae that clustering gene expression data groups together efficiently genes of known similar function, and we find a similar tendency in human data. Thus patterns seen in genome-wide expression experiments can be interpreted as indications of the status of cellular processes. Also, coexpression of genes of known function with poorly characterized or novel genes may provide a simple means of gaining leads to the functions of many genes for which information is not available currently.

L18 ANSWER 3 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1999:277453 BIOSIS
DOCUMENT NUMBER: PREV199900277453
TITLE: Analysis of gene expression data using self-organizing maps.
AUTHOR(S): Toronen, Petri; Kolehmainen, Mikko; Wong, Garry; Castren, Eero (1)
CORPORATE SOURCE: (1) A.I. Virtanen Institute, University of Kuopio, 70211, Kuopio Finland
SOURCE: FEBS Letters, (May 21, 1999) Vol. 451, No. 2, pp. 142-146. ISSN: 0014-5793.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

AB DNA **microarray** technologies together with rapidly increasing genomic sequence information is leading to an explosion in available gene expression data. Currently there is a great need for efficient methods to analyze and visualize these massive data sets. A self-organizing map (SOM) is an unsupervised neural network learning algorithm which has been successfully used for the analysis and organization of large data files. We have here applied the SOM algorithm to analyze published data of yeast gene expression and show that SOM is an excellent tool for the analysis and visualization of gene expression profiles.

L18 ANSWER 4 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1999:57519 BIOSIS
DOCUMENT NUMBER: PREV199900057519
TITLE: **Cluster analysis** and display of genome-wide expression patterns.
AUTHOR(S): Eisen, Michael B.; Spellman, Paul T.; Brown, Patrick O.; Botstein, David (1)

CORPORATE SOURCE: (1) Dep. Genetics, Stanford Univ. Sch. Med., 300 Pasteur Ave., Stanford, CA 94305 USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (Dec., 1998) Vol. 95, No. 25, pp. 14863-14868.
ISSN: 0027-8424.
DOCUMENT TYPE: Article
LANGUAGE: English
AB A system of **cluster analysis** for genome-wide expression data from DNA **microarray** hybridization is described that uses standard statistical algorithms to arrange genes according to similarity in pattern of gene expression. The output is displayed graphically, conveying the clustering and the underlying expression data simultaneously in a form intuitive for biologists. We have found in the budding yeast Saccharomyces cerevisiae that clustering gene expression data groups together efficiently genes of known similar function, and we find a similar tendency in human data. Thus patterns seen in genome-wide expression experiments can be interpreted as indications of the status of cellular processes. Also, coexpression of genes of known function with poorly characterized or novel genes may provide a simple means of gaining leads to the functions of many genes for which information is not available currently.

L18 ANSWER 5 OF 8 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:616046 CAPLUS
DOCUMENT NUMBER: 131:332905
TITLE: **Cluster analysis** and display of genome-wide expression patterns. [Erratum to document cited in CA130:163878]
AUTHOR(S): Eisen, Michael B.; Spellman, Paul T.; Brown, Patrick O.; Botstein, David
CORPORATE SOURCE: Dep. Genetics, Howard Hughes Medical Institute, Stanford Univ. School Medicine, Stanford, CA, 94305, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1999), 96(19), 10943
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Two refs. were omitted. Ref. 1 [Weinstein, J. N., Myers, T. G., O'Connor, P. M., Friend, S. H., Fornace, A. J., Jr., Kohn, K. W., Fojo, T., Bates, S. E., Rubinstein, L. V., Anderson, N. L., et al. (1997) science 275, 343-349] refers to a precedent for coloring of data tables following cluster anal. Ref. 2 [Wen, X., Fuhrman, S., Michaels, G. S., Carr, D. B., Smith, S., Barker, J. L Somogyi, R. (1998) Proc. Natl. Acad. Sci. USA 95, 334-339] refers to an earlier example of applying cluster anal. to gene expression data.
REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1998:805587 CAPLUS
DOCUMENT NUMBER: 130:163878
TITLE: **Cluster analysis** and display of genome-wide expression patterns
AUTHOR(S): Eisen, Michael B.; Spellman, Paul T.; Brown, Patrick O.; Botstein, David
CORPORATE SOURCE: Department of Genetics, Howard Hughes Medical Institute, Stanford University School of Medicine, Stanford, CA, 94305, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1998), 95(25), 14863-14868
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A system of cluster anal. for genome-wide expression data from DNA **microarray** hybridization is described that uses std. statistical algorithms to arrange genes according to similarity in pattern of gene expression. The output is displayed graphically, conveying the clustering and the underlying expression data simultaneously in a form intuitive for biologists. We have found in the budding yeast Saccharomyces cerevisiae that clustering gene expression data groups together efficiently genes of known similar function, and we find a similar tendency in human data. Thus patterns seen in genome-wide expression expts. can be interpreted as indications of the status of cellular processes. Also, coexpression of genes of known function with poorly characterized or novel genes may provide a simple means of gaining leads to the functions of many genes for which information is not available currently.
REFERENCE COUNT: 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 7 OF 8 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 1999175621 EMBASE
TITLE: Analysis of gene expression data using self-organizing maps.
AUTHOR: Toronen P.; Kolehmainen M.; Wong G.; Castren E.
CORPORATE SOURCE: E. Castren, A.I. Virtanen Institute, University of Kuopio, 70211 Kuopio, Finland. eero.castren@uku.fi
SOURCE: FEBS Letters, (1999) 451/2 (142-146).
Refs: 13
ISSN: 0014-5793 CODEN: FEBLAL
PUBLISHER IDENT.: S 0014-5793(99)00524-4
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 002 Physiology
022 Human Genetics
027 Biophysics, Bioengineering and Medical Instrumentation
029 Clinical Biochemistry
004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English
AB DNA **microarray** technologies together with rapidly increasing genomic sequence information is leading to an explosion in available gene expression data. Currently there is a great need for efficient methods to analyze and visualize these massive data sets. A self-organizing map (SOM) is an unsupervised neural network learning algorithm which has been successfully used for the analysis and organization of large data files. We have here applied the SOM algorithm to analyze published data of yeast gene expression and show that SOM is an excellent tool for the analysis and visualization of gene expression profiles. Copyright (C) 1999 Federation of European Biochemical Societies.

L18 ANSWER 8 OF 8 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 1999002839 EMBASE
TITLE: **Cluster analysis** and display of genome-wide expression patterns.
AUTHOR: Eisen M.B.; Spellman P.T.; Brown P.O.; Botstein D.
CORPORATE SOURCE: D. Botstein, Department of Genetics, Howard Hughes Medical Institute, Stanford Univ. School of Medicine, 300 Pasteur Avenue, Stanford, CA 94305, United States. botstein@genome.stanford.edu
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1998) 95/25 (14863-14868).
Refs: 16
ISSN: 0027-8424 CODEN: PNASA6

COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
LANGUAGE: English
SUMMARY LANGUAGE: English
AB A system of **cluster analysis** for genome-wide expression data from DNA **microarray** hybridization is described that uses standard statistical algorithms to arrange genes according to similarity in pattern of gene expression. The output is displayed graphically, conveying the clustering and the underlying expression data simultaneously in a form intuitive for biologists. We have found in the budding yeast Saccharomyces cerevisiae that clustering gene expression data groups together efficiently genes of known similar function, and we find a similar tendency in human data. Thus patterns seen in genome-wide expression experiments can be interpreted as indications of the status of cellular processes. Also, coexpression of genes of known function with poorly characterized or novel genes may provide a simple means of gaining leads to the functions of many genes for which information is not available currently.

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L1             0 TORONEN P/IN

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'IN' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'MEDLINE'
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E1             1     TORONDZHADZE G I/IN
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E5             1     TORONTALI STEVEN J/IN
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E7             1     TORONYI ANDRAS/IN
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E1          13     CASTRANTAS HARRY M/IN
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E3           0 --> CASTREN E/IN
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E5           1     CASTREN EINO/IN
E6           1     CASTRESANA MAXIMO I/IN
E7           3     CASTRESANA PELAYO JOSE MARIA/IN
E8           1     CASTRIC P/IN
E9           2     CASTRIC PETER/IN
E10          3     CASTRICUM M/IN
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L2           1 CASTREN EERO/IN

=> d l2

L2   ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2002 ACS
AN   1996:563521  CAPLUS
DN   125:186667
TI   Methods of promoting the survival and differentiation of subclasses of
     cholinergic and serotonergic neurons using fibroblast growth factor-5.
IN   Lindholm, Dan B. W.; Hartikka, Jukka A.; Berzaghi, Maria D.; Castren,
     Eero; Tzimagiorgis, Georgios; Hughes, Richard A.; Thoenen, Hans
PA   Max-Planck-Gesellschaft zur Forderung der Wissenschaften E.V., Germany
SO   S. African, 58 pp.
     CODEN: SFXXAB
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.        KIND  DATE          APPLICATION NO.  DATE
     ---------------   ----  --------      ---------------  --------
PI   ZA 9409535         A    19950814      ZA 1994-9535     19941130
PRAI US 1993-160307          19931201


=> s castren eino/in
'IN' IS NOT A VALID FIELD CODE
'IN' IS NOT A VALID FIELD CODE
L3           1 CASTREN EINO/IN

=> d l3

L3   ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2002 ACS
AN   1928:26202  CAPLUS
DN   22:26202
OREF 22:3045c-d
TI   Conical wood-chip distributor for chemical pulp boilers
IN   Castren, Eino; Oksa, Einari
DT   Patent
LA   Unavailable
FAN.CNT 1
     PATENT NO.        KIND  DATE          APPLICATION NO.  DATE
     ---------------   ----  --------      ---------------  --------
PI   US 1675211              19280626      US
```

```
=> s microarray
L4       12481 MICROARRAY

=> s analysis
L5     6009867 ANALYSIS

=> s data
L6     4713394 DATA

=> s l4 and l5
L7        5996 L4 AND L5

=> s l6 and l7
L8        1833 L6 AND L7

=> s l8 not py>1999
L9          96 L8 NOT PY>1999

=> s cluster
L10     234950 CLUSTER

=> s l9 and l10
L11         10 L9 AND L10

=> dup rem
ENTER L# LIST OR (END):l11
PROCESSING COMPLETED FOR L11
L12           5 DUP REM L11 (5 DUPLICATES REMOVED)

=> d l12

L12  ANSWER 1 OF 5  CAPLUS  COPYRIGHT 2002 ACS
AN   1999:616046  CAPLUS
DN   131:332905
TI   Cluster analysis and display of genome-wide expression
     patterns. [Erratum to document cited in CA130:163878]
AU   Eisen, Michael B.; Spellman, Paul T.; Brown, Patrick O.; Botstein, David
CS   Dep. Genetics, Howard Hughes Medical Institute, Stanford Univ. School
     Medicine, Stanford, CA, 94305, USA
SO   Proceedings of the National Academy of Sciences of the United States of
     America (1999), 96(19), 10943
     CODEN: PNASA6; ISSN: 0027-8424
PB   National Academy of Sciences
DT   Journal
LA   English
RE.CNT  2     THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L12  ANSWER 1 OF 5  CAPLUS  COPYRIGHT 2002 ACS
AN   1999:616046  CAPLUS
DN   131:332905
TI   Cluster analysis and display of genome-wide expression
     patterns. [Erratum to document cited in CA130:163878]
AU   Eisen, Michael B.; Spellman, Paul T.; Brown, Patrick O.; Botstein, David
CS   Dep. Genetics, Howard Hughes Medical Institute, Stanford Univ. School
     Medicine, Stanford, CA, 94305, USA
SO   Proceedings of the National Academy of Sciences of the United States of
     America (1999), 96(19), 10943
     CODEN: PNASA6; ISSN: 0027-8424
PB   National Academy of Sciences
```

DT Journal
LA English
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2002 ACS
AN 1999:551900 CAPLUS
DN 131:194891
TI Present status and problems of DNA **microarray** informatics
AU Eguchi, Yukihiro
CS Res. Inst., Mitsui Knowledge Ind. Co., Ltd., Japan
SO Jikken Igaku (1999), 17(13), 1670-1673
CODEN: JIIGEF; ISSN: 0288-5514
PB Yodosha
DT Journal; General Review
LA Japanese

L12 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2002 ACS
AN 1999:365095 CAPLUS
DN 131:195430
TI Clustering **analysis** for gene expression **data**
AU Chen, Yidong; Ermolaeva, Olga; Bittner, Michael L.; Meltzer, Paul; Trent, Jeffrey; Dougherty, Edward R.; Batman, Sinan
CS National Human Genome Research Inst., National Institutes of Health, Bethesda, MD, USA
SO Proceedings of SPIE-The International Society for Optical Engineering (1999), 3602(Advances in Fluorescence Sensing Technology IV), 422-428
CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 4 OF 5 MEDLINE DUPLICATE 1
AN 1999297564 MEDLINE
DN 99297564 PubMed ID: 10371154
TI **Analysis** of gene expression **data** using self-organizing maps.
AU Toronen P; Kolehmainen M; Wong G; Castren E
CS A.I. Virtanen Institute, University of Kuopio, Finland.
SO FEBS LETTERS, (1999 May 21) 451 (2) 142-6.
Journal code: EUH; 0155157. ISSN: 0014-5793.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199907
ED Entered STN: 19990715
Last Updated on STN: 19990715
Entered Medline: 19990706

L12 ANSWER 5 OF 5 MEDLINE DUPLICATE 2
AN 1999061959 MEDLINE
DN 99061959 PubMed ID: 9843981
TI **Cluster analysis** and display of genome-wide expression patterns.
AU Eisen M B; Spellman P T; Brown P O; Botstein D
CS Department of Genetics, Stanford University School of Medicine, 300 Pasteur Avenue, Stanford, CA 94305, USA.
NC CA46406 (NCI)
CA77097 (NCI)
HG00983 (NHGRI)
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF